

FORM PTO-1390 (Modified) (REV 10-95)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER <u>01123.0004</u>
TRANSMITTAL LETTER TO THE UNITED STATES		DESIGNATED/ELECTED OFFICE (DO/EO/US)		U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR 09/509712
CONCERNING A FILING UNDER 35 U.S.C. 371				
INTERNATIONAL APPLICATION NO. PCT/US98/21276	INTERNATIONAL FILING DATE 8 October 1998		PRIORITY DATE CLAIMED 10 October 1997	
TITLE OF INVENTION MAMMALIAN GENES INVOLVED IN VIRAL INFECTION AND TUMOR SUPPRESSION				
APPLICANT(S) FOR DO/EO/US RUBIN, Donald H.; ORGAN, Edward L.; DUBOIS, Raymond N.				
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:				
<ol style="list-style-type: none"> 1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371. 2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. 3. <input checked="" type="checkbox"/> This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1). 4. <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date. 5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371 (c) (2)) <ol style="list-style-type: none"> a. <input type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau). b. <input type="checkbox"/> has been transmitted by the International Bureau. c. <input checked="" type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). 6. <input type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371(c)(2)). 7. <input type="checkbox"/> A copy of the International Search Report (PCT/ISA/210). 8. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371 (c)(3)) <ol style="list-style-type: none"> a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau). b. <input type="checkbox"/> have been transmitted by the International Bureau. c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. d. <input checked="" type="checkbox"/> have not been made and will not be made. 9. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). 10. <input checked="" type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)). 11. <input type="checkbox"/> A copy of the International Preliminary Examination Report (PCT/IPEA/409). 12. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371 (c)(5)). 				
Items 13 to 18 below concern document(s) or information included:				
<ol style="list-style-type: none"> 13. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98. 14. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included. 15. <input checked="" type="checkbox"/> A FIRST preliminary amendment. A SECOND or SUBSEQUENT preliminary amendment. 16. <input type="checkbox"/> A substitute specification. 17. <input type="checkbox"/> A change of power of attorney and/or address letter. 18. <input checked="" type="checkbox"/> Certificate of Mailing by Express Mail 19. <input checked="" type="checkbox"/> Other items or information: 				
Check in the amount of \$943.00 for filing fees; return-receipt postcard; Certificate of Express Mailing No. EL348124625US ; Verified Statements Claiming Small Entity Status signed by Vanderbilt University and by Avatar BioSci, Inc.				

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR 09/509712	INTERNATIONAL APPLICATION NO. PCT/US98/21276	ATTORNEY'S DOCKET NUMBER 01123.0004		
20. The following fees are submitted:		CALCULATIONS PTO USE ONLY		
BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) :				
<input checked="" type="checkbox"/> Search Report has been prepared by the EPO or JPO \$840.00 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) \$670.00 <input type="checkbox"/> No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)) \$760.00 <input type="checkbox"/> Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$970.00 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) \$96.00				
ENTER APPROPRIATE BASIC FEE AMOUNT =		\$840.00		
Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 CFR 1.492 (e)).		<input type="checkbox"/> 20 <input type="checkbox"/> 30 \$0.00		
CLAIMS		NUMBER FILED	NUMBER EXTRA	RATE
Total claims	29	- 20 =	9	x \$18.00 \$162.00
Independent claims	11	- 3 =	8	x \$78.00 \$624.00
Multiple Dependent Claims (check if applicable).		<input checked="" type="checkbox"/>		\$260.00
TOTAL OF ABOVE CALCULATIONS		=		\$1,886.00
Reduction of 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28) (check if applicable).		<input checked="" type="checkbox"/>		\$943.00
SUBTOTAL		=		\$943.00
Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 CFR 1.492 (f)).		<input type="checkbox"/> 20 <input type="checkbox"/> 30	+ \$0.00	
TOTAL NATIONAL FEE		=		\$943.00
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) (check if applicable).		<input type="checkbox"/>	\$0.00	
TOTAL FEES ENCLOSED		=		\$943.00
		Amount to be: refunded		\$
		charged		\$

A check in the amount of **\$943.00** to cover the above fees is enclosed.

Please charge my Deposit Account No. _____ in the amount of _____ to cover the above fees.
A duplicate copy of this sheet is enclosed.

The Commissioner is hereby authorized to charge any fees which may be required, or credit any overpayment to Deposit Account No. **14-0629** A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

Janice A. Kimpel, Ph.D.
NEEDLE & ROSENBERG, P.C.
127 Peachtree Street, N.E., Suite 1200
Atlanta, Georgia 30303 U.S.A.
(404) 688 0770


SIGNATURE

Janice A. Kimpel

NAME

42,734

REGISTRATION NUMBER

March 30, 2000
DATE

09/509712
430 Rec'd PCT/PTO 3-1 MAR 2000

CERTIFICATE OF EXPRESS MAILING

I hereby certify that the filing of the U.S. National Phase in the names of Rubin *et al.*, consisting of: Transmittal Letter to the United States Designated/Elected Office (DO/EO/US) Concerning a Filing Under 35 U.S.C. 371 (2 pages), a check in the amount of \$943.00 for filing fee, Verified Statement Claiming Small Entity Status by Vanderbilt University (2 pages), Verified Statement Claiming Small Entity Status by Avatar BioSci, Inc. (2 pages), Declaration/Power of Attorney by Rubin, Organ & Dubois and return-receipt postcard are being deposited with the United States Postal Service as Express Mail No. EL348124625US in an envelope addressed to: Box PCT, Assistant Commissioner for Patents, Washington, D.C., 20231, on this **30th** day of **March 2000**.



Everardo McFarlane

3-30-2000

Date

ATTORNEY DOCKET NO. 01123.0004
PAGE 1 OF 2

Applicant or Patentee: Donald H. Rubin, Edward L. Organ and Raymond N. Dubois

For: **"MAMMALIAN GENES INVOLVED IN VIRAL
INFECTION AND TUMOR SUPPRESSION"****VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY
STATUS (37 CFR 1.9(f) and 1.27(d)) - SMALL BUSINESS CONCERN**

I hereby declare that I am

the owner of the small business concern identified below:
 an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN: Avatar Biosci, Inc.
ADDRESS OF CONCERN: 1937 Edenbridge Way
Nashville, TN 37215

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18(d), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled "**MAMMALIAN GENES INVOLVED IN VIRAL INFECTION AND TUMOR SUPPRESSION**" by inventor(s) Donald H. Rubin, Edward L. Organ and Raymond N. Dubois described in the specification filed concurrently herewith.

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below* and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR 1.9(d) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

*

W053858.WPD

ATTORNEY DOCKET NO. 01123.0004
PAGE 2 OF 2

*NOTE: Separate verified statements are required for each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

NAME: VANDERBILT UNIVERSITY

ADDRESS: Office of Technology Transfer
1207 17th Ave. S., Suite 210
Nashville, TN 37212

INDIVIDUAL SMALL BUSINESS CONCERN NONPROFIT ORGANIZATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING:

Donald H Rubin

TITLE IN ORGANIZATION:

President

ADDRESS OF PERSON SIGNING:

Avatar Biosci, Inc.
1937 Edenbridge Way
Nashville, TN 37215

SIGNATURE

Dr. Donald H. Rubin

DATE

3.28.00

ATTORNEY DOCKET NO. 01123.0004

APPLICANT OR PATENTEE: Donald H. Rubin, Edward L. Organ and Raymond N. Dubois
FOR: "MAMMALIAN GENES INVOLVED IN VIRAL
 INFECTION AND TUMOR SUPPRESSION"

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY
 STATUS (37 CFR 1.9(f) and 1.27(d)) - NONPROFIT ORGANIZATION**

I hereby declare that I am an official empowered to act on behalf of the nonprofit organization identified below:

NAME OF ORGANIZATION: VANDERBILT UNIVERSITY
ADDRESS OF ORGANIZATION: Office of Technology Transfer
 1207 17th Ave. S., Suite 210
 Nashville, TN 37212

TYPE OF ORGANIZATION:

- University or other institution of higher education
 (Name of state: Tennessee
 (Citation of statute: _____))
- Tax exempt under Internal Revenue Service Code (26 USC 501(a) and 501(c)(3))
- Non-profit scientific or educational under statute of state of the United States of America
 (Name of state _____)
 (Citation of statute _____))
- Would qualify as tax exempt under Internal Revenue Service Code (26 USC 501(a) and 501(c)(3)) if it were located in The United States of America
- Would qualify as nonprofit scientific or educational under statute of state of The United States of America if it were located in The United States of America
 (Name of state _____)
 (Citation of statute _____))

I hereby declare that the nonprofit organization identified above qualifies as a nonprofit organization as defined in 37 CFR 1.9 (e) for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code with regard to the invention entitled "MAMMALIAN GENES INVOLVED IN VIRAL INFECTION AND TUMOR SUPPRESSION" by inventor(s) Donald H. Rubin, Edward L. Organ and Raymond N. Dubois filed concurrently herewith.

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit organization with regard to the above identified invention.

If the rights held by the nonprofit organization are not exclusive, each individual, concern or organization having rights to the invention is listed below* and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR

1.9(d) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

*NOTE: Separate verified statements are required for each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

NAME Avatar Biosci, Inc.

ADDRESS 1937 Edenbridge Way
Nashville, TN 37215

INDIVIDUAL SMALL BUSINESS CONCERN NONPROFIT ORGANIZATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: JANIS ELSNER

TITLE IN ORGANIZATION: ASSOC. DIRECTOR

ADDRESS OF PERSON SIGNING:
Vanderbilt University
Office of Technology Transfer
1207 17th Ave. S., Suite 210
Nashville, TN 37212

SIGNATURE: Janis Elsner

DATE: Mar 29, 2000

09/509712
430 Rec'd PCT/PTO 3-1 MAR 2000

ATTORNEY DOCKET NO. 01123.0004
PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of :
: *Rubin, Donald H. et al.*
Serial No.: Unassigned : Group Art Unit: Unassigned
Filed: Concurrently herewith : Examiner: Unassigned
For: **“MAMMALIAN GENES INVOLVED
IN VIRAL INFECTION AND
TUMOR SUPPRESSION”** :

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

NEEDLE & ROSENBERG, P.C.
Suite 1200, The Candler Building
127 Peachtree Street, N.E.
Atlanta, Georgia 30303-1811

March 30, 2000

Sir:

Concurrently with the filing of this application, Applicants respectfully request entry of the following amendment:

IN THE SPECIFICATION:

On Page 1, at line 3 immediately after the title “Mammalian Genes Involved in Viral Infection and Tumor Suppression”, please insert the following:

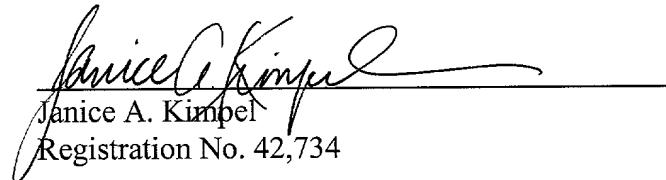
“This invention was made with partial government support under National Institutes of Health Grant No. CA68283 and a grant from the Department of Veterans Affairs. The United States Government has certain rights in the invention.”

ATTORNEY DOCKET NO. 01123.0004
PATENT

No fee is believed due; however, the Commissioner is hereby authorized to charge any deficiency to Deposit Account No. 14-0629.

Respectfully submitted,

NEEDLE & ROSENBERG, P.C.

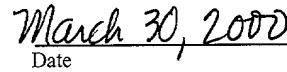

Janice A. Kimpel
Registration No. 42,734

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Suite 1200, The Candler Building
127 Peachtree Street, N.E.
Atlanta, Georgia 30303-1811
404/688-0770

CERTIFICATE OF EXPRESS MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as Express Mailing No. EL348124625US in an envelope addressed to: Assistant Commissioner for Patents, Box PCT, Washington, D.C. 20231, on this 30th day of March, 2000.


Janice A. Kimpel


Date

MAMMALIAN GENES INVOLVED IN VIRAL INFECTION
AND TUMOR SUPPRESSION

BACKGROUND

Field of the Invention

The present invention provides methods of identifying cellular genes used for 5 viral growth or for tumor progression. Thus, the present invention relates to nucleic acids related to and methods of reducing or preventing viral infection and for suppressing tumor progression. The invention also relates to methods for screening for additional such genes.

Background art

10 Various projects have been directed toward isolating and sequencing the genome of various animals, notably the human. However, most methodologies provide nucleotide sequences for which no function is linked or even suggested, thus limiting the immediate usefulness of such data.

15 The present invention, in contrast, provides methods of screening only for nucleic acids that are involved in a specific process, *i.e.*, viral infection or tumor progression. For viral infection, the nucleic acids isolated are useful in treatments for these processes because by this method only nucleic acids which are also nonessential to the cell are isolated. Such methods are highly useful, since they ascribe a function to each isolated gene, and thus the isolated nucleic acids can immediately be utilized in various specific 20 methods and procedures.

25 For, example, the present invention provides methods of isolating nucleic acids encoding gene products used for viral infection, but nonessential to the cell. Viral infections are significant causes of human morbidity and mortality. Understanding the molecular mechanisms of such infections will lead to new approaches in their treatment and control.

Viruses can establish a variety of types of infection. These infections can be 30 generally classified as lytic or persistent, though some lytic infections are considered persistent. Generally, persistent infections fall into two categories: (1) chronic (productive) infection, *i.e.*, infection wherein infectious virus is present and can be recovered by traditional biological methods and (2) latent infection, *i.e.*, infection

wherein viral genome is present in the cell but infectious virus is generally not produced except during intermittent episodes of reactivation. Persistence generally involves stages of both productive and latent infection.

Lytic infections can also persist under conditions where only a small fraction of the total cells are infected (smoldering (cycling) infection). The few infected cells release virus and are killed, but the progeny virus again only infect a small number of the total cells. Examples of such smoldering infections include the persistence of lactic dehydrogenase virus in mice (Mahy, B.W.J., *Br. Med. Bull.* 41: 50-55 (1985)) and adenovirus infection in humans (Porter, D.D. pp. 784-790 in Baron, S., ed. *Medical Microbiology* 2d ed. (Addison-Wesley, Menlo Park, CA 1985)).

Furthermore, a virus may be lytic for some cell types but not for others. For example, evidence suggests that human immunodeficiency virus (HIV) is more lytic for T cells than for monocytes/macrophages, and therefore can result in a productive infection of T cells that can result in cell death, whereas HIV-infected mononuclear phagocytes may produce virus for considerable periods of time without cell lysis. (Klatzmann, et al. *Science* 225:59-62 (1984); Koyanagi, et al. *Science* 241:1673-1675 (1988); Sattentau, et al. *Cell* 52:631-633 (1988)).

Traditional treatments for viral infection include pharmaceuticals aimed at specific virus derived proteins, such as HIV protease or reverse transcriptase, or recombinant (cloned) immune modulators (host derived), such as the interferons. However, the current methods have several limitations and drawbacks which include high rates of viral mutations which render anti-viral pharmaceuticals ineffective. For immune modulators, limited effectiveness, limiting side effects, a lack of specificity all limit the general applicability of these agents. Also the rate of success with current antivirals and immune-modulators has been disappointing.

One aspect of the current invention focuses on isolating genes that are not essential for cellular survival when disrupted in one or both alleles, but which are required for virus replication. This may occur with a dose effect, in which one allele knock-out may confer the phenotype of virus resistance for the cell. As targets for therapeutic intervention, inhibition of these cellular gene products, including: proteins, parts of proteins (modification enzymes that include, but are not restricted to glycosylation, lipid modifiers [myriolate, etc.]), lipids, transcription elements and RNA

regulatory molecules, may be less likely to have profound toxic side effects and virus mutation is less likely to overcome the 'block' to replicate successfully.

The present invention provides a significant improvement over previous methods of attempted therapeutic intervention against viral infection by addressing the cellular genes required by the virus for growth. Therefore, the present invention also provides an innovative therapeutic approach to intervention in viral infection by providing methods to treat viruses by inhibiting the cellular genes necessary for viral infection. Because these genes, by virtue of the means by which they are originally detected, are nonessential to the cell's survival at a level of expression necessary to inhibit virus replication, these treatment methods can be used in a subject without serious detrimental effects to the subject, as has been found with previous methods. The present invention also provides the surprising discovery that virally infected cells are dependent upon a factor in serum to survive. Therefore, the present invention also provides a method for treating viral infection by inhibiting this serum survival factor. Finally, these discoveries also provide a novel method for removing virally infected cells from a cell culture by removing, inhibiting or disrupting this serum survival factor in the culture so that non-infected cells selectively survive.

The selection of tumor suppressor gene(s) has become an important area in the discovery of new target for therapeutic intervention of cancer. Since the discovery that cells are restricted from promiscuous entry into the cell cycle by specific genes that are capable of suppressing a 'transformed' phenotype, considerable time has been invested in the discovery of such genes. Some of these genes include the gene associated by rhabdomyosarcoma (Rb) and the p53 (apoptosis related) encoding gene. The present invention provides a method, using gene-trapping, to select cell lines that have a transformed phenotype from cells that are not transformed and to isolate from these cells a gene that can suppress a malignant, or transformed, phenotype. Thus, by the nature of the isolation process, a function is associated with the isolated genes. The capacity to select quickly tumor suppressor genes can provide unique targets in the process of treating or preventing, and even for diagnostic testing of, cancer.

DETAILED DESCRIPTION OF THE INVENTION

The present invention utilizes a "gene trap" method along with a selection process to identify and isolate nucleic acids from genes associated with a particular function. Specifically, it provides a means of isolating cellular genes necessary for viral infection but not essential for the cell's survival, and it provides a means of isolating cellular genes that suppress tumor progression.

The present invention also provides a core discovery that virally infected cells become dependent upon at least one factor present in serum for survival, whereas non-infected cells do not exhibit this dependence. This core discovery has been utilized in the present invention in several ways. First, inhibition of the "serum survival factor" can be utilized to eradicate persistently virally infected cells from populations of non-infected cells. Inhibition of this factor can also be used to treat virus infection in a subject, as further described herein. Additionally, inhibition of or withdrawal of the serum survival factor in tissue culture allows for the detection of cellular genes required for viral replication yet nonessential for an uninfected cell to survive. The present invention further provides several such cellular genes, as well as methods of treating viral infections by inhibiting the functioning of such genes.

The invention also provides cellular genes whose overexpression is associated with inhibition of viral growth and/or reproduction.

The present method provides several cellular genes that are necessary for viral growth in the cell but are not essential for the cell to survive. These genes are important for lytic and persistent infection by viruses. These genes were isolated by generating gene trap libraries by infecting cells with a retrovirus gene trap vector, selecting for cells in which a gene trap event occurred (*i.e.*, in which the vector had inserted such that the promoterless marker gene was inserted such that a cellular promoter promotes transcription of the marker gene, *i.e.*, inserted into a functioning gene), starving the cells of serum, infecting the selected cells with the virus of choice while continuing serum starvation, and adding back serum to allow visible colonies to develop, which colonies were cloned by limiting dilution. Genes into which the retrovirus gene trap vector inserted were then isolated from the colonies using probes specific for the retrovirus gene trap vector. Thus nucleic acids isolated by this method are isolated portions of genes. Additionally, utilizing this method, several cellular genes were isolated whose

overexpression prevents viral infection or tumor growth, and they provide methods of treating viral infection or tumor growth/suppression by overexpression of these genes.

Thus the present invention provides a method of identifying a cellular gene necessary for viral growth in a cell and nonessential for cellular survival, comprising (a) transferring into a cell culture, *e.g.* growing in serum-containing medium, a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, (c) removing serum from the culture medium, (d) infecting the cell culture with the virus, and (e) isolating from the surviving cells a cellular gene within which the marker gene is inserted, thereby identifying a gene necessary for viral growth in a cell and nonessential for cellular survival. The present invention also provides a method of identifying a cellular gene used for viral growth in a cell and nonessential for cellular survival, comprising (a) transferring into a cell culture growing in serum-containing medium a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, (c) removing serum from the culture medium, (d) infecting the cell culture with the virus, and (e) isolating from the surviving cells a cellular gene within which the marker gene is inserted, thereby identifying a gene necessary for viral growth in a cell and nonessential for cellular survival or a gene whose overexpression prevents viral reproduction but is not fatal to the survival of the cell. In any selected cell type, such as Chinese hamster ovary cells, one can readily determine if serum starvation is required for selection. If it is not, serum starvation may be eliminated from the steps.

Alternatively, instead of removing serum from the culture medium, a serum factor required by the virus for growth can be inhibited, such as by the administration of an antibody that specifically binds that factor. Furthermore, if it is believed that there are no persistently infected cells in the culture, the serum starvation step can be eliminated and the cells grown in usual medium for the cell type. If serum starvation is used, it can be continued for a time after the culture is infected with the virus. Serum can then be added back to the culture. If some other method is used to inactivate the factor, it can be discontinued, inactivated or removed (such as removing the anti-factor antibody, *e.g.*, with a bound antibody directed against that antibody) prior to adding fresh serum back to the culture. Cells that survive are mutants having an inactivating insertion in a gene necessary for growth of the virus. The genes having the insertions can then be isolated by isolating sequences having the marker gene sequences. This mutational process

disturbs a wild type function. A mutant gene may produce at a lower level a normal product, it may produce a normal product not normally found in these cells, it may cause the overproduction of a normal product, it may produce an altered product that has some functions but not others, or it may completely disrupt a gene function. Additionally, the 5 mutation may disrupt an RNA that has a function but is never translated into a protein. For example, the alpha-tropomyosin gene has a 3' RNA that is very important in cell regulation but never is translated into protein. (*Cell* 75 pg 1107-1117, 12/17/93).

As used herein, a cellular gene "nonessential for cellular survival" means a gene for which disruption of one or both alleles results in a cell viable for at least a period of 10 time which allows viral replication to be inhibited for preventative or therapeutic uses or use in research. A gene "necessary for viral growth" means the gene product, either protein or RNA, secreted or not, is necessary or beneficial, either directly or indirectly in some way for the virus to grow, and therefore, in the absence of that gene product (*i.e.*, a functionally available gene product), the virus does not spread. For example, such genes 15 can encode cell cycle regulatory proteins, proteins affecting the vacuolar hydrogen pump, or proteins involved in protein folding and protein modification, including but not limited to: phosphorylation, methylation, glycosylation, myristylation or other lipid moiety, or protein processing via enzymatic processing. Some examples of such genes include vacuolar H⁺ATPase, alpha tropomyosin, gas5 gene, ras complex, N-acetyl- 20 glucosaminy-l-transferase I mRNA, annexin II, c-golgi CM130 and calcyclin.

Any virus capable of infecting the cell can be used for this method. Virus can be selected based upon the particular infection desired to study. However, it is contemplated by the present invention that many viruses will be dependent upon the same cellular genes for survival; thus a cellular gene isolated using one virus can be used 25 as a target for therapy for other viruses as well. Any cellular gene can be tested for relevancy to any desired virus using the methods set forth herein, *i.e.*, in general, by inhibiting the gene or its gene product in a cell and determining if the desired virus can grow in that cell. Some examples of viruses include HIV (including HIV-1 and HIV-2); parvovirus; papillomaviruses; hantaviruses; influenza viruses (*e.g.*, influenza A, B and C 30 viruses); hepatitis viruses A to G; caliciviruses; astroviruses; rotaviruses; coronaviruses, such as human respiratory coronavirus; picornaviruses, such as human rhinovirus and enterovirus; ebola virus; human herpesvirus (*e.g.*, HSV-1-9); human adenovirus; for animal, the animal counterpart to any above listed human virus, animal retroviruses, such

as simian immunodeficiency virus, avian immunodeficiency virus, bovine immunodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, caprine arthritis encephalitis virus, arenaviruses, arboviruses, tickborne viruses or visna virus.

5 The nucleic acids comprising cellular genes of this invention were isolated by the above method and as set forth in the examples. The invention includes a nucleic acid comprising the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:15, 10 SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, 15 SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, 20 SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:112, SEQ 25 ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, and SEQ ID NO:127 (this list is sometimes referred to herein as "SEQ LIST 1" for brevity). Thus these nucleic acids can contain, in addition to the nucleotides set forth in each SEQ ID NO in the sequence listing, additional nucleotides at either end of the molecule. Such additional nucleotides can be added by 30 any standard method, as known in the art, such as recombinant methods and synthesis methods. Examples of such nucleic acids comprising the nucleotide sequence set forth in any entry of the sequence listing contemplated by this invention include, but are not limited to, for example, the nucleic acid placed into a vector; a nucleic acid having one or

more regulatory region (e.g., promoter, enhancer, polyadenylation site) linked to it, particularly in functional manner, *i.e.* such that an mRNA or a protein can be produced; a nucleic acid including additional nucleic acids of the gene, such as a larger or even full length genomic fragment of the gene, a partial or full length cDNA, a partial or full length RNA. Making and/or isolating such larger nucleic acids is further described below and is well known and standard in the art.

Also provided in this invention are the double-stranded nucleic acids corresponding to the nucleic acid sequences set forth in SEQ ID 1 through SEQ ID 136, inclusive. It is recognized that "nucleic acid" as used herein, can refer to either or both 10 strands of such double-stranded nucleic acids, such strands often referred to as the "positive" and "negative" strands. Either strand of such double-stranded nucleic acids may encode the polypeptides of this invention, and the coding sequences for such polypeptides may be translated in either direction along the strand. Examples of polypeptides encoded by either strand are disclosed herein.

15 The invention also provides a nucleic acid encoding the protein encoded by the gene comprising the nucleotide sequence set forth in any of the sequences listed in SEQ LIST 1, as well as allelic variants and homologs of each such gene. The gene is readily obtained using standard methods, as described below and as is known and standard in the art. The present invention also contemplates any unique fragment of these genes or of 20 the nucleic acids set forth in any of the sequences listed in SEQ LIST 1. Examples of inventive fragments of the inventive genes can include the nucleic acids whose sequence is set forth in any of the sequences listed in SEQ LIST 1. To be unique, the fragment must be of sufficient size to distinguish it from other known sequences, most readily determined by comparing any nucleic acid fragment to the nucleotide sequences of 25 nucleic acids in computer databases, such as GenBank. Such comparative searches are standard in the art. Typically, a unique fragment useful as a primer or probe will be at least about 20 to about 25 nucleotides in length, depending upon the specific nucleotide content of the sequence. Additionally, fragments can be, for example, at least about 30, 40, 50, 75, 100, 200 or 500 nucleotides in length. The nucleic acids can be single or 30 double stranded, depending upon the purpose for which it is intended.

The present invention further provides a nucleic acid comprising the regulatory region of a gene comprising any one of the nucleotide sequences set forth in SEQ LIST 1, as well as homologs of each such gene. Additionally provided is a construct

comprising such a regulatory region functionally linked to a reporter gene. Such reporter gene constructs can be used to screen for compounds and compositions that affect expression of the gene comprising the nucleic acids whose sequence is set forth in SEQ LIST 1, or any homologs thereof.

5 The nucleic acids set forth in the sequence listing are gene fragments; the entire coding sequence and the entire gene that comprises each fragment are both contemplated herein and are readily obtained by standard methods, given the nucleotide sequences presented in the sequence listing (see, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989; *DNA cloning: A Practical Approach*, Volumes I and II, Glover, D.M. ed., IRL Press Limited, Oxford, 1985). To obtain the entire genomic gene, briefly, a nucleic acid whose sequence is set forth in any of SEQ ID NO:1 through SEQ ID NO:127, or preferably in any of the sequences listed in SEQ LIST 1, or a smaller fragment thereof, is utilized as a probe to screen a genomic library under high stringency conditions, and 10 isolated clones are sequenced. Once the sequence of the new clone is determined, a probe can be devised from a portion of the new clone not present in the previous fragment and hybridized to the library to isolate more clones containing fragments of the gene. In this manner, by repeating this process in organized fashion, one can "walk" along the chromosome and eventually obtain nucleotide sequence for the entire gene. 15 Similarly, one can use portions of the present fragments, or additional fragments obtained from the genomic library, that contain open reading frames to screen a cDNA library to obtain a cDNA having the entire coding sequence of the gene. Repeated screens can be utilized as described above to obtain the complete sequence from several clones if necessary. The isolates can then be sequenced to determine the nucleotide 20 sequence by standard means such as dideoxynucleotide sequencing methods (see, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989).

30 The present genes were isolated from rat; however, homologs in any desired species, preferably mammalian, such as human, can readily be obtained by screening a human library, genomic or cDNA, with a probe comprising sequences of the nucleic acids set forth in the sequence listing herein, or fragments thereof, and isolating genes specifically hybridizing with the probe under preferably relatively high stringency hybridization conditions. For example, high salt conditions (e.g., in 6X SSC or 6X

SSPE) and/or high temperatures of hybridization can be used. For example, the stringency of hybridization is typically about 5°C to 20°C below the T_m (the melting temperature at which half of the molecules dissociate from its partner) for the given chain length. As is known in the art, the nucleotide composition of the hybridizing region factors in determining the melting temperature of the hybrid. For 20mer probes, for example, the recommended hybridization temperature is typically about 55-58°C. Additionally, the rat sequence can be utilized to devise a probe for a homolog in any specific animal by determining the amino acid sequence for a portion of the rat protein, and selecting a probe with optimized codon usage to encode the amino acid sequence of the homolog in that particular animal. Any isolated gene can be confirmed as the targeted gene by sequencing the gene to determine it contains the nucleotide sequence listed herein as comprising the gene. Any homolog can be confirmed as a homolog by its functionality.

Additionally contemplated by the present invention are nucleic acids, from any desired species, preferably mammalian and more preferably human, having 98%, 95%, 90%, 85%, 80%, 70%, 60%, or 50% homology, or greater, in the region of homology, to a region in an exon of a nucleic acid encoding the protein encoded by the gene comprising the nucleotide sequence set forth in any of the sequences listed in SEQ LIST 1 or to homologs thereof. Also contemplated by the present invention are nucleic acids, from any desired species, preferably mammalian and more preferably human, having 98%, 95%, 90%, 85%, 80%, 70%, 60%, or 50% homology, or greater, in the region of homology, to a region in an exon of a nucleic acid comprising the nucleotide sequence set forth in any of the sequences listed in SEQ LIST 1 or to homologs thereof. These genes can be synthesized or obtained by the same methods used to isolate homologs, with stringency of hybridization and washing, if desired, reduced accordingly as homology desired is decreased, and further, depending upon the G-C or A-T richness of any area wherein variability is searched for. Allelic variants of any of the present genes or of their homologs can readily be isolated and sequenced by screening additional libraries following the protocol above. Methods of making synthetic genes are described in U.S. Patent No. 5,503,995 and the references cited therein.

The nucleic acid encoding any selected protein of the present invention can be any nucleic acid that functionally encodes that protein. For example, to functionally encode, *i.e.*, allow the nucleic acid to be expressed, the nucleic acid can include, for

example, exogenous or endogenous expression control sequences, such as an origin of replication, a promoter, an enhancer, and necessary information processing sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Preferred expression control sequences can be promoters derived

5 from metallothionein genes, actin genes, immunoglobulin genes, CMV, SV40, adenovirus, bovine papilloma virus, etc. Expression control sequences can be selected for functionality in the cells in which the nucleic acid will be placed. A nucleic acid encoding a selected protein can readily be determined based upon the amino acid sequence of the selected protein, and, clearly, many nucleic acids will encode any selected

10 protein.

The present invention additionally provides a nucleic acid that selectively hybridizes under stringent conditions with a nucleic acid set forth in SEQ LIST 1 or with a nucleic acid encoding the protein encoded by the gene comprising the nucleotide sequence set forth in any sequence listed in SEQ LIST 1. This hybridization can be

15 specific. The degree of complementarity between the hybridizing nucleic acid and the sequence to which it hybridizes should be at least enough to exclude hybridization with a nucleic acid encoding an unrelated protein. Thus, a nucleic acid that selectively hybridizes with a nucleic acid of the present protein coding sequence will not selectively hybridize under stringent conditions with a nucleic acid for a different, unrelated protein,

20 and vice versa. Typically, the stringency of hybridization to achieve selective hybridization involves hybridization in high ionic strength solution (6X SSC or 6X SSPE) at a temperature that is about 12-25°C below the T_m (the melting temperature at which half of the molecules dissociate from its partner) followed by washing at a combination of temperature and salt concentration chosen so that the washing temperature is about 5°C

25 to 20°C below the T_m of the hybrid molecule. The temperature and salt conditions are readily determined empirically in preliminary experiments in which samples of reference DNA immobilized on filters are hybridized to a labeled nucleic acid of interest and then washed under conditions of different stringencies. Hybridization temperatures are typically higher for DNA-RNA and RNA-RNA hybridizations. The washing

30 temperatures can be used as described above to achieve selective stringency, as is known in the art. (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989; Kunkel et al. *Methods Enzymol.* 1987:154:367, 1987). Nucleic acid fragments that selectively hybridize to any

given nucleic acid can be used, *e.g.*, as primers and or probes for further hybridization or for amplification methods (*e.g.*, polymerase chain reaction (PCR), ligase chain reaction (LCR)). A preferable stringent hybridization condition for a DNA:DNA hybridization can be at about 68°C (in aqueous solution) in 6X SSC or 6X SSPE followed by washing 5 at 68°C.

The present invention additionally provides a polypeptide comprising the amino acid sequence encoded by the gene comprising the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ 10 ID NO:13, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID 15 NO:45, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID 20 NO:80, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, 25 SEQ ID NO:112, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, and SEQ ID NO:127 (*i.e.*, SEQ LIST 1). Additionally, polypeptides comprising the amino acid sequence encoded by a nucleic acid that selectively hybridizes under stringent conditions with a nucleic acid in SEQ LIST 1 are provided. Further, polypeptides comprising the amino acid sequence 30 encoded by a nucleic acid having a region within an exon wherein the region has at least 50, 60, 70, 80, 90, or 95% homology with a nucleic acid in SEQ LIST 1. These polypeptides can be readily obtained by any of several means. For example, the nucleotide sequence of coding regions of the gene can be translated and then the

corresponding polypeptide can be synthesized mechanically by standard methods. Additionally, the coding regions of the genes can be expressed or synthesized, an antibody specific for the resulting polypeptide can be raised by standard methods (see, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor 5 Laboratory, Cold Spring Harbor, New York, 1988), and the protein can be isolated from other cellular proteins by selective hybridization with the antibody. This protein can be purified to the extent desired by standard methods of protein purification (see, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989). The amino acid sequence of 10 any protein, polypeptide or peptide of this invention can be deduced from the nucleic acid sequence, or it can be determined by sequencing an isolated or recombinantly produced protein.

The terms "peptide," "polypeptide" and "protein" can be used interchangeably herein and refer to a polymer of amino acids and includes full-length proteins and 15 fragments thereof. As used in the specification and in the claims, "a" can mean one or more, depending upon the context in which it is used. An amino acid residue is an amino acid formed upon chemical digestion (hydrolysis) of a polypeptide at its peptide linkages. The amino acid residues described herein are preferably in the L isomeric form. However, residues in the D isomeric form can be substituted for any L-amino acid 20 residue, as long as the desired functional property is retained by the polypeptide. Standard polypeptide nomenclature (described in *J. Biol. Chem.*, 243:3552-59 (1969) and adopted at 37 CFR § 1.822(b)) is used herein.

As will be appreciated by those skilled in the art, the invention also includes those polypeptides having slight variations in amino acid sequences or other properties. Amino 25 acid substitutions can be selected by known parameters to be neutral (see, e.g., Robinson WE Jr, and Mitchell WM., AIDS 4:S151-S162(1990)). Such variations may arise naturally as allelic variations (e.g., due to genetic polymorphism) or may be produced by human intervention (e.g., by mutagenesis of cloned DNA sequences), such as induced point, deletion, insertion and substitution mutants. Minor changes in amino acid 30 sequence are generally preferred, such as conservative amino acid replacements, small internal deletions or insertions, and additions or deletions at the ends of the molecules. Substitutions may be designed based on, for example, the model of Dayhoff, *et al.* (in *Atlas of Protein Sequence and Structure* 1978, Nat'l Biomed. Res. Found., Washington,

D.C.). These modifications can result in changes in the amino acid sequence, provide silent mutations, modify a restriction site, or provide other specific mutations. Likewise, such amino acid changes result in a different nucleic acid encoding the polypeptides and proteins. Thus, alternative nucleic acids are also contemplated by such modifications.

5 The present invention also provides cells containing a nucleic acid of the invention. A cell containing a nucleic acid encoding a protein typically can replicate the DNA and, further, typically can express the encoded protein. The cell can be a prokaryotic cell, particularly for the purpose of producing quantities of the nucleic acid, or a eukaryotic cell, particularly a mammalian cell. The cell is preferably a mammalian
10 10 cell for the purpose of expressing the encoded protein so that the resultant produced protein has mammalian protein processing modifications.

Nucleic acids of the present invention can be delivered into cells by any selected means, in particular depending upon the purpose of the delivery of the compound and the target cells. Many delivery means are well-known in the art. For example,
15 15 electroporation, calcium phosphate precipitation, microinjection, cationic or anionic liposomes, and liposomes in combination with a nuclear localization signal peptide for delivery to the nucleus can be utilized, as is known in the art.

The present invention also contemplates that the mutated cellular genes necessary for viral growth, produced by the present method, as well as cells containing these
20 20 mutants can also be useful. These mutated genes and cells containing them can be isolated and/or produced according to the methods herein described and using standard methods.

It should be recognized that the sequences set forth herein may contain minor sequencing errors. Such errors can be corrected, for example, by using the hybridization
25 25 procedure described above with various probes derived from the described sequences such that the coding sequence can be reisolated and resequenced.

As described in the examples, the present invention provides the discovery of a "serum survival factor" present in serum that is necessary for the survival of persistently virally infected cells. Isolation and characterization of this factor have shown it to be a
30 30 protein, to have a molecular weight of between about 50 kD and 100 kD, to resist inactivation in low pH (e.g., pH2) and chloroform extraction, to be inactivated by boiling for about 5 minutes and in low ionic strength solution (e.g., about 10 mM to about 50 mM). The present invention thus provides a purified mammalian serum protein having a

molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which when removed from a cell culture comprising cells persistently infected with reovirus selectively substantially prevents

5 survival of cells persistently infected with reovirus. The factor, fitting the physical characteristics described above, can readily be verified by adding it to non-serum-containing medium (which previously could not support survival of persistently virally infected cells) and determining whether this medium with the added putative factor can now support persistently virally infected cells, particularly cells persistently infected with

10 reovirus. As used herein, a "purified" protein means the protein is at least of sufficient purity such that an approximate molecular weight can be determined.

The amino acid sequence of the protein can be elucidated by standard methods. For example, an antibody to the protein can be raised and used to screen an expression library to obtain nucleic acid sequence coding the protein. This nucleic acid sequence is

15 then simply translated into the corresponding amino acid sequence. Alternatively, a portion of the protein can be directly sequenced by standard amino acid sequencing methods (amino-terminus sequencing). This amino acid sequence can then be used to generate an array of nucleic acid probes that encompasses all possible coding sequences for a portion of the amino acid sequence. The array of probes is used to screen a cDNA

20 library to obtain the remainder of the coding sequence and thus ultimately the corresponding amino acid sequence.

The present invention also provides methods of detecting and isolating additional serum survival factors. For example, to determine if any known serum components are necessary for viral growth, the known components can be inhibited in, or eliminated

25 from, the culture medium, and it can be observed whether viral growth is inhibited by determining if persistently infected cells do not survive. One can add the factor back (or remove the inhibition) and determine whether the factor allows for viral growth.

Additionally, other, unknown serum components can also be found to be essential for growth. Serum can be fractionated by various standard means, and fractions added to

30 serum free medium to determine if a factor is present in a reaction that allows growth previously inhibited by the lack of serum. Fractions having this activity can then be further fractionated until the factor is relatively free of other components. The factor can then be characterized by standard methods, such as size fractionation, denaturation and/or

inactivation by various means, etc. Preferably, once the factor has been purified to a desired level of purity, it is added to cells in serum free medium to confirm that it bestows the function of allowing virus to grow when serum-free medium alone did not. This method can be repeated to confirm the requirement for the specific factor for any desired 5 virus, since each serum factor found to be required by any one virus can also be required by many other viruses. In general, the closer the viruses are related and the more similar the infection modes of the viruses, the more likely that a factor required by one virus will be required by the other.

The present invention also provides methods of treating virus infections utilizing 10 applicants' discoveries. The subject of any of the herein described methods can be any animal, preferably a mammal, such as a human, a veterinary animal, such as a cat, dog, horse, pig, goat, sheep, or cow, or a laboratory animal, such as a mouse, rat, rabbit, or guinea pig, depending upon the virus.

The present invention provides a method of reducing or inhibiting, and thereby 15 treating, a viral infection in a subject, comprising administering to the subject an inhibiting amount of a composition that inhibits functioning of the serum protein described herein, *i.e.* the serum protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength 20 solution, and which when removed from a cell culture comprising cells persistently infected with the virus prevents survival of at least some cells persistently infected with the virus, thereby treating the viral infection. The composition can comprise, for example, an antibody that specifically binds the serum protein, or an antisense RNA that binds an RNA encoded by a gene functionally encoding the serum protein.

25 Any virus capable of infecting the selected subject to be treated can be treated by the present methods. As described above, any serum protein or survival factor found by the present methods to be necessary for growth of cells infected with any one virus can be found to be necessary for growth of the cells infected with many other viruses. For any given cell-virus combination, the serum protein or factor can be confirmed to be required 30 for growth by the methods described herein. The cellular genes identified by the examples using reovirus, a mammalian pathogen, and a rat cell system have general applicability to other virus infections that include all of the known as well as yet to be discovered human pathogens, including, but not limited to: human immunodeficiency

viruses (e.g., HIV-1, HIV-2); parvovirus; papillomaviruses; hantaviruses; influenza viruses (e.g., influenza A, B and C viruses); hepatitis viruses A to G; caliciviruses; astroviruses; rotaviruses; coronaviruses, such as human respiratory coronavirus; picornaviruses, such as human rhinovirus and enterovirus; ebola virus; human

5 herpesvirus (e.g., HSV-1-9); human adenovirus; hantaviruses; for animal, the animal counterpart to any above listed human virus, animal retroviruses, such as simian immunodeficiency virus, avian immunodeficiency virus, bovine immunodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, caprine arthritis encephalitis virus, arenaviruses, arboviruses, tickborne virus or visna virus.

10 A protein inhibiting amount of the composition can be readily determined, such as by administering varying amounts to cells or to a subject and then adjusting the effective amount for inhibiting the protein according to the volume of blood or weight of the subject. Compositions that bind to the protein can be readily determined by running the putatively bound protein on a protein gel and observing an alteration in the protein's

15 migration through the gel. Inhibition of the protein can be determined by any desired means such as adding the inhibitor to complete media used to maintain persistently infected cells and observing the cells' viability. The composition can comprise, for example, an antibody that specifically binds the serum protein. Specific binding by an antibody means that the antibody can be used to selectively remove the factor from serum

20 or inhibit the factor's biological activity and can readily be determined by radio immune assay (RIA), bioassay, or enzyme-linked immunosorbant (ELISA) technology. The composition can comprise, for example, an antisense RNA that specifically binds an RNA encoded by the gene encoding the serum protein. Antisense RNAs can be synthesized and used by standard methods (e.g., *Antisense RNA and DNA*, D. A. Melton, Ed., Cold

25 Spring Harbor Laboratory, Cold Spring Harbor, NY (1988)).

The present methods provide a method of screening a compound for effectiveness in treating or preventing a viral infection, comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product necessary for reproduction of the virus in the cell but not necessary for survival of the cell and detecting the level

30 and/or activity (i.e. function) of the gene product produced, a decrease or elimination of the gene product and/or the gene product activity indicating a compound for treating or preventing the viral infection. The cellular gene can be, for example, a nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ

ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82; SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, or SEQ ID NO:127 (herein sometimes referred to as SEQ LIST 2, for brevity), any homolog thereof, or any other gene obtained using the methods provided herein for obtaining such genes. It is understood that the cellular gene can be present naturally in the cell being screened, or it can be introduced into the cell in a suitable expression vector, as are well known in the art. The level of the gene product can be measured by any standard means, such as by detection with an antibody specific for the protein. The level of gene product can be compared to the level of the gene product in a control cell not contacted with the compound. The level of gene product can be compared to the level of the gene product in the same cell prior to addition of the compound. Activity, or function, can be measured by any standard means, such as by enzymatic assays that measure the conversion of a substrate to a product or binding

assays that measure the binding of a protein to a nucleic acid, for example. Examples of gene products disclosed herein whose activity/function can be measured include tristetraprolin (human ZFP-36), 6-pyruvoyl-tetrahydropterin synthase, a eukaryotic DnaJ-like protein, ID3 (inhibitor of DNA binding 3), N-acetylglucos-aminyltransferase I (mGAT-1), cleavage stimulation factor (CSTF2), TAK1 binding protein, human zinc transcription factor ZPF207, Dlx2, Smad7 (Mad-related protein), and P-glycoprotein (mdr1b). The activity can be compared to the activity in a control cell not contacted with the compound or in the same cell prior to addition of the compound. Relatedly, the regulatory region of the gene can be functionally linked to a reporter gene and compounds can be screened for inhibition of the reporter gene. Such reporter constructs are described herein.

The present invention also provides a method of screening a compound for effectiveness in treating or preventing a viral infection comprising contacting the compound with the gene product of a cellular gene comprising a nucleic acid of SEQ LIST 2, or any homolog thereof, and detecting the function of the gene product, a decrease or elimination of the function indicating a compound effective for treating or preventing viral infection. Examples of gene products disclosed herein that can be utilized in this method include tristetraprolin (human ZFP-36), 6-pyruvoyl-tetrahydropterin synthase, a eukaryotic DnaJ-like protein, ID3 (inhibitor of DNA binding 3), N-acetylglucos-aminyltransferase I (mGAT-1), cleavage stimulation factor (CSTF2), TAK1 binding protein, human zinc transcription factor ZPF207, Dlx2, Smad7 (Mad-related protein), and P-glycoprotein (mdr1b).

The present invention provides a method of selectively eliminating cells persistently infected with a virus from an animal cell culture capable of surviving for a first period of time in the absence of serum, comprising propagating the cell culture in the absence of serum for a second time period during which a persistently infected cell cannot survive without serum, thereby selectively eliminating from the cell culture cells persistently infected with the virus. The second time period should be shorter than the first time period. Thus one can simply eliminate serum from a standard culture medium composition for a period of time (e.g. by removing serum containing medium from the culture container, rinsing the cells, and adding serum-free medium back to the container), then, after a time of serum starvation, return serum to the culture medium. Alternatively, one can inhibit a serum survival factor from the culture in place of the step of serum starvation. Furthermore, one can instead interfere with the virus-factor interaction. Such a

viral elimination method can periodically be performed for cultured cells to ensure that they remain virus-free. The time period of serum removal can greatly vary, with a typical range being about 1 to about 30 days; a preferable period can be about 3 to about 10 days, and a more preferable period can be about 5 days to about 7 days. This time period can be

5 selected based upon ability of a specific cell to survive without serum as well as the life cycle of the target virus, *e.g.*, for reovirus, which has a life cycle of about 24 hours, 3 days' starvation of cells provides dramatic results.

Furthermore, the time period can be shortened by also passaging the cells during the starvation; in general, increasing the number of passages can decrease the time of

10 serum starvation (or serum factor inhibition) needed to get full clearance of the virus from the culture. While passaging, the cells typically are exposed briefly to serum (typically for about 3 to about 24 hours). This exposure both stops the action of the trypsin used to dislodge the cells and stimulates the cells into another cycle of growth, thus aiding in this selection process. Thus a starvation/serum cycle can be repeated to optimize the selective

15 effect. Other standard culture parameters, such as confluence of the cultures, pH, temperature, etc. can be varied to alter the needed time period of serum starvation (or serum survival factor inhibition). This time period can readily be determined for any given viral infection by simply removing the serum for various periods of time, then testing the cultures for the presence of the infected cells (*e.g.*, by ability to survive in the

20 absence of serum and confirmed by quantitating virus in cells by standard virus titration and immunohistochemical techniques) at each tested time period, and then detecting at which time periods of serum deprivation the virally infected cells were eliminated. It is preferable that shorter time periods of serum deprivation that still provide elimination of the persistently infected cells be used. Furthermore, the cycle of starvation, then adding

25 back serum and determining amount of virus remaining in the culture can be repeated until no virtually infected cells remain in the culture.

Thus, the present method can further comprise passaging the cells, *i.e.*, transferring the cell culture from a first container to a second container. Such transfer can facilitate the selective lack of survival of virally infected cells. Transfer can be repeated several times.

30 Transfer is achieved by standard methods of tissue culture (*see, e.g.*, Freshney, *Culture of Animal Cells, A Manual of Basic Technique*, 2nd Ed. Alan R. Liss, Inc., New York, 1987).

The present method further provides a method of selectively eliminating from a cell culture cells persistently infected with a virus, comprising propagating the cell culture

in the absence of a functional form of the serum protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which when removed from a cell culture comprising cells

5 persistently infected with reovirus substantially prevents survival of cells persistently infected with reovirus. The absence of the functional form can be achieved by any of several standard means, such as by binding the protein to an antibody selective for it (binding the antibody in serum either before or after the serum is added to the cells; if before, the serum protein can be removed from the serum by, e.g., binding the antibody to

10 a column and passing the serum over the column and then administering the survival protein-free serum to the cells), by administering a compound that inactivates the protein, or by administering a compound that interferes with the interaction between the virus and the protein.

Thus, the present invention provides a method of selectively eliminating from a

15 cell culture propagated in serum-containing medium cells persistently infected with a virus, comprising inhibiting in the serum the protein having a molecular weight of between about 50 kD and 100 kD which resists inactivation in low pH and resists inactivation by chloroform extraction, which inactivates when boiled and inactivates in low ionic strength solution, and which when removed from a cell culture comprising cells persistently

20 infected with reovirus substantially prevents survival of cells persistently infected with reovirus. Alternatively, the interaction between the virus and the serum protein can be disrupted to selectively eliminate cells persistently infected with the virus.

Any virus capable of some form of persistent infection may be eliminated from a cell culture utilizing the present elimination methods, including removing, inhibiting or

25 otherwise interfering with a serum protein, such as the one exemplified herein, and also including removing, inhibiting or otherwise interfering with a gene product from any cellular gene found by the present method to be necessary for viral growth yet nonessential to the cell. For example, DNA viruses or RNA viruses can be targeted. One can readily determine whether cells infected with a selected virus can be selectively removed from a

30 culture through removal of serum by starving cells permissive to the virus of serum (or inhibiting the serum survival factor), adding the selected virus to the cells, adding serum to the culture, and observing whether infected cells die (*i.e.*, by titering levels of virus in the surviving cells with an antibody specific for the virus).

A culture of any animal cell (*i.e.*, any cell that is typically grown and maintained in culture in serum) that can be maintained for a period of time in the absence of serum, can be purified from viral infection utilizing the present method. For example, primary cultures as well as established cultures and cell lines can be used. Furthermore, cultures of 5 cells from any animal and any tissue or cell type within that animal that can be cultured and that can be maintained for a period of time in the absence of serum can be used. For example, cultures of cells from tissues typically infected, and particularly persistently infected, by an infectious virus could be used.

As used in the claims "in the absence of serum" means at a level at which 10 persistently virally infected cells do not survive. Typically, the threshold level is about 1% serum in the media. Therefore, about 1% serum or less can be used, such as about 1%, 0.75%, 0.50%, 0.25% 0.1% or no serum can be used.

As used herein, "selectively eliminating" cells persistently infected with a virus means that substantially all of the cells persistently infected with the virus are killed such 15 that the presence of virally infected cells cannot be detected in the culture immediately after the elimination procedure has been performed. Furthermore, "selectively eliminating" includes that cells not infected with the virus are generally not killed by the method. Some surviving cells may still produce virus but at a lower level, and some may be defective in pathways that lead to death by the virus. Typically, for cells persistently 20 infected with virus to be substantially all killed, more than about 90% of the cells, and more preferably more than about 95%, 98%, 99%, or 99.99% of virus-containing cells in the culture are killed.

The present method also provides a nucleic acid comprising the regulatory region of any of the genes. Such regulatory regions can be isolated from the genomic sequences 25 isolated and sequenced as described above and identified by any characteristics observed that are characteristic for regulatory regions of the species and by their relation to the start codon for the coding region of the gene. The present invention also provides a construct comprising the regulatory region functionally linked to a reporter gene. Such constructs are made by routine subcloning methods, and many vectors are available into which 30 regulatory regions can be subcloned upstream of a marker gene. Marker genes can be chosen for ease of detection of marker gene product.

The present method therefore also provides a method of screening a compound for treating a viral infection, comprising administering the compound to a cell containing any

of the above-described constructs, comprising a regulatory region of one of the genes comprising any of the nucleotide sequences set forth in SEQ LIST 2, or any homologs thereof, whose inhibition or reduction in expression causes inhibition of viral replication wherein the region is functionally linked to a reporter gene, and detecting the level of the

5 reporter gene product produced, a decrease or elimination of the reporter gene product indicating a compound for treating the viral infection. Compounds detected by this method would inhibit transcription of the gene from which the regulatory region was isolated, and thus, in treating a subject, would inhibit the production of the gene product produced by the gene, and thus treat the viral infection.

10 Some genes when disrupted by the present method of retrovirus insertion, resulted in over expression of the gene product, and this overexpression inhibited viral replication. Thus the present invention provides a method of screening a compound for effectiveness in treating a viral infection, comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product whose overexpression inhibits

15 reproduction of the virus but does not prevent survival of the cell and detecting the level of the gene product produced, an increase in the gene product indicating a compound effective for treating the viral infection. Typically, an increase will be a 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 175%, 200%, 300%, 400%, 500% or higher increase over gene product produced when the compound is not present.

20 The present invention additionally provides a method of reducing or inhibiting a viral infection in a subject, comprising administering to the subject an amount of a composition that inhibits expression or functioning of a gene product encoded by a gene comprising the nucleic acid set forth in any of SEQ LIST 2, or a homolog thereof, thereby treating the viral infection. Reducing or inhibiting viral infection naturally can include

25 both the initial infection of the subject and the infection of uninfected cells within an already infected subject, e.g. inhibiting viral replication in cells of the subject. The composition can comprise, for example, an antibody that binds a protein encoded by the gene. The composition can also comprise an antibody that binds a receptor for a protein encoded by the gene. Such an antibody can be raised against the selected protein by

30 standard methods as set forth above, and can be either polyclonal or monoclonal, though monoclonal is preferred. Alternatively, the composition can comprise an antisense RNA that binds an RNA encoded by the gene, as described above. Examples of antisense RNA useful therapeutically include the fragments of the nucleic acids described above.

Furthermore, the composition can comprise a nucleic acid functionally encoding an antisense RNA that binds an RNA encoded by the gene. Other useful compositions will be readily apparent to the skilled artisan.

The present invention also provides a method of treating a viral infection in a subject comprising administering to the subject a treatment effective amount of a composition that increases expression of a gene whose over expression reduces or inhibits viral replication. Typically, an increase will be a 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 175%, 200%, 300%, 400%, 500% or higher increase over gene product produced when the composition is not present.

10 The present invention further provides a method of reducing or inhibiting a viral infection in a subject comprising mutating *ex vivo* in a selected cell, for example from the subject or from an allogenic source, an endogenous gene comprising a nucleic acid set forth in SEQ LIST 2 whose inhibition or reduction in expression causes inhibition of viral replication, or a homolog thereof, to a gene form incapable of producing a functional gene product of the gene or a gene form producing a reduced amount of a functional gene product of the gene, and placing (or replacing, in the case of the subject's own cells) the cell in the subject, thereby reducing viral infection of cells in the subject. The cell can be selected according to the typical target cell of the specific virus whose infection is to be reduced, prevented or inhibited. A preferred cell for several viruses is a hematopoietic cell. When the selected cell is a hematopoietic cell, viruses which can be reduced or inhibited from infection can include, for example, HIV, including HIV-1 and HIV-2. However, many other virus-cell combinations will be apparent to the skilled artisan.

The invention also includes a method of reducing or inhibiting viral infection in a subject comprising mutating *ex vivo* in a selected cell, for example from a subject or an allogenic source, an endogenous gene comprising a nucleic acid set forth in SEQ LIST 2 whose overexpression causes inhibition of viral replication, or a homolog thereof, to a gene form that expresses the gene at a higher level than the endogenous gene, and placing or replacing the cell in the subject. Typically, a higher level can be 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 175%, 200%, 300%, 400%, 500% or higher than the non-mutated, endogenous gene. The cell can be selected according to the typical target cell of the specific virus whose infection is to be reduced, prevented or inhibited. A preferred cell for several viruses is a hematopoietic cell. When the selected cell is a hematopoietic cell, viruses which can be reduced or inhibited from infection can

include, for example, HIV, including HIV-1 and HIV-2. However, many other virus-cell combinations will be apparent to the skilled artisan.

The present invention additionally provides a method of increasing viral infection resistance in a subject comprising mutating *ex vivo* in a selected cell, for example from the 5 subject or from an allogenic source, an endogenous gene comprising a nucleic acid set forth in SEQ LIST 2, whose inhibition or reduction in expression increases viral infection resistance, said endogenous gene being mutated to a mutated gene form incapable of producing a functional gene product of the gene or a gene form producing a reduced amount of a functional gene product of the gene, and placing the cell in the subject, 10 thereby increasing viral infection resistance of cells in the subject. The virus can be HIV, particularly when the cell is a hematopoietic cell. However, many other virus-cell combinations will be apparent to the skilled artisan.

Furthermore, the present invention provides a method for isolation of cellular genes utilized in tumor progression. The present invention provides a method of identifying a 15 cellular gene that can suppress a malignant phenotype in a cell, comprising (a) transferring into a cell culture incapable of growing well in soft agar or Matrigel a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, and (c) isolating from selected cells which are capable of growing in soft agar or Matrigel a cellular gene within which the marker gene is inserted, thereby 20 identifying a gene that can suppress a malignant phenotype in a cell. This method can be performed using any selected non-transformed cell line, of which many are known in the art.

The present invention additionally provides a method of identifying a cellular gene that can suppress a malignant phenotype in a cell, comprising (a) transferring into a cell 25 culture of non-transformed cells a vector encoding a selective marker gene lacking a functional promoter, (b) selecting cells expressing the marker gene, and (c) isolating from selected and transformed cells a cellular gene within which the marker gene is inserted, thereby identifying a gene that can suppress a malignant phenotype in a cell. A non-transformed phenotype can be determined by any of several standard methods in the 30 art, such as the exemplified inability to grow in soft agar, or inability to grow in Matrigel.

The present invention further provides a method of screening for a compound for suppressing a malignant phenotype in a cell comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product involved in

establishment of a malignant phenotype in the cell and detecting the level of the gene product produced, a decrease, inhibition or elimination of the gene product indicating a compound effective for suppressing the malignant phenotype. Detection of the level, or amount, of gene product produced can be measured, directly or indirectly, by any of 5 several methods standard in the art (e.g., protein gel, antibody-based assay, detecting labeled RNA) for assaying protein levels or amounts, and selected based upon the specific gene product.

The present invention also provides a method of screening for a compound for suppressing a malignant phenotype in a cell comprising administering the compound to a 10 cell containing a cellular gene functionally encoding a gene product whose overexpression is involved in suppressing a malignant phenotype in the cell and detecting the level of the gene product produced, an increase in the gene product indicating a compound effective for suppressing the malignant phenotype.

The present invention further provides a method of suppressing a malignant 15 phenotype in a cell in a subject, comprising administering to the subject an amount of a composition that inhibits expression or functioning of a gene product encoded by a gene comprising the nucleic acid set forth in SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:36 or SEQ ID NO:94, or a homolog thereof, or any gene whose overexpression is found by the present method to be 20 involved in suppressing a malignant phenotype in the cell (e.g., any clone designated herein with an "x") thereby suppressing a malignant phenotype. The composition can, for example, comprise an antibody that binds a protein encoded by the gene. The composition can, as another example, comprise an antibody that binds a receptor for a protein encoded by the gene. The composition can comprise an antisense RNA that binds an RNA 25 encoded by the gene. Further, the composition can comprise a nucleic acid functionally encoding an antisense RNA that binds an RNA encoded by the gene.

The present invention further provides a method of suppressing a malignant phenotype in a cell in a subject, comprising administering to the subject an amount of a composition that increases expression of a gene product whose overexpression is involved 30 in suppressing a malignant phenotype in the cell. The gene product can be the product of a gene wherein disruption of an upstream gene by the present vector resulted in overexpression of the downstream gene, and the overexpression of the downstream gene

demonstrated a transformed phenotype. The composition can be, for example, an inhibitor, such as a small molecule inhibitor, of the COX 2 enzyme.

Diagnostic or therapeutic agents of the present invention can be administered to a subject or an animal model by any of many standard means for administering therapeutics or diagnostics to that selected site or standard for administering that type of functional entity. For example, an agent can be administered orally, parenterally (e.g., intravenously), by intramuscular injection, by intraperitoneal injection, topically, transdermally, or the like. Agents can be administered, *e.g.*, as a complex with cationic liposomes, or encapsulated in anionic liposomes. Compositions can include various amounts of the selected agent in combination with a pharmaceutically acceptable carrier and, in addition, if desired, may include other medicinal agents, pharmaceutical agents, carriers, adjuvants, diluents, etc. Parental administration, if used, is generally characterized by injection. Injectables can be prepared in conventional forms, either as liquid solutions or suspensions, solid forms suitable for solution or suspension in liquid prior to injection, or as emulsions. Depending upon the mode of administration, the agent can be optimized to avoid degradation in the subject, such as by encapsulation, etc.

Dosages will depend upon the mode of administration, the disease or condition to be treated, and the individual subject's condition, but will be that dosage typical for and used in administration of antiviral or anticancer agents. Dosages will also depend upon the composition being administered, *e.g.*, a protein or a nucleic acid. Such dosages are known in the art. Furthermore, the dosage can be adjusted according to the typical dosage for the specific disease or condition to be treated. Furthermore, viral titers in culture cells of the target cell type can be used to optimize the dosage for the target cells *in vivo*, and transformation from varying dosages achieved in culture cells of the same type as the target cell type can be monitored. Often a single dose can be sufficient; however, the dose can be repeated if desirable. The dosage should not be so large as to cause adverse side effects. Generally, the dosage will vary with the age, condition, sex and extent of the disease in the patient and can be determined by one of skill in the art. The dosage can also be adjusted by the individual physician in the event of any complication.

For administration to a cell in a subject, the composition, once in the subject, will of course adjust to the subject's body temperature. For *ex vivo* administration, the composition can be administered by any standard methods that would maintain viability of the cells, such as by adding it to culture medium (appropriate for the target cells) and

adding this medium directly to the cells. As is known in the art, any medium used in this method can be aqueous and non-toxic so as not to render the cells non-viable. In addition, it can contain standard nutrients for maintaining viability of cells, if desired. For *in vivo* administration, the complex can be added to, for example, a blood sample or a tissue

5 sample from the patient, or to a pharmaceutically acceptable carrier, e.g., saline and buffered saline, and administered by any of several means known in the art. Examples of administration include parenteral administration, e.g., by intravenous injection including regional perfusion through a blood vessel supplying the tissue(s) or organ(s) having the target cell(s), or by inhalation of an aerosol, subcutaneous or intramuscular injection,

10 topical administration such as to skin wounds and lesions, direct transfection into, e.g., bone marrow cells prepared for transplantation and subsequent transplantation into the subject, and direct transfection into an organ that is subsequently transplanted into the subject. Further administration methods include oral administration, particularly when the composition is encapsulated, or rectal administration, particularly when the composition is

15 in suppository form. A pharmaceutically acceptable carrier includes any material that is not biologically or otherwise undesirable, i.e., the material may be administered to an individual along with the selected complex without causing any undesirable biological effects or interacting in a deleterious manner with any of the other components of the pharmaceutical composition in which it is contained.

20 Specifically, if a particular cell type *in vivo* is to be targeted, for example, by regional perfusion of an organ or tumor, cells from the target tissue can be biopsied and optimal dosages for import of the complex into that tissue can be determined *in vitro*, as described herein and as known in the art, to optimize the *in vivo* dosage, including concentration and time length. Alternatively, cultured cells of the same cell type can also

25 be used to optimize the dosage for the target cells *in vivo*.

For either *ex vivo* or *in vivo* use, the complex can be administered at any effective concentration. An effective concentration is that amount that results in reduction, inhibition or prevention of the viral infection or in reduction or inhibition of the transformed phenotype of the cells.

30 A nucleic acid can be administered in any of several means, which can be selected according to the vector utilized, the organ or tissue, if any, to be targeted, and the characteristics of the subject. The nucleic acids, if desired in a pharmaceutically acceptable carrier such as physiological saline, can be administered systemically, such as

intravenously, intraarterially, orally, parenterally, subcutaneously. The nucleic acids can also be administered by direct injection into an organ or by injection into the blood vessel supplying a target tissue. For an infection of cells of the lungs or trachea, it can be administered intratracheally. The nucleic acids can additionally be administered topically, 5 transdermally, etc.

The nucleic acid or protein can be administered in a composition. For example, the composition can comprise other medicinal agents, pharmaceutical agents, carriers, adjuvants, diluents, etc. Furthermore, the composition can comprise, in addition to the vector, lipids such as liposomes, such as cationic liposomes (e.g., DOTMA, DOPE, 10 DC-cholesterol) or anionic liposomes. Liposomes can further comprise proteins to facilitate targeting a particular cell, if desired. Administration of a composition comprising a vector and a cationic liposome can be administered to the blood afferent to a target organ or inhaled into the respiratory tract to target cells of the respiratory tract. Regarding liposomes, see, e.g., Brigham et al. *Am. J. Resp. Cell. Mol. Biol.* 1:95-100 15 (1989); Felgner et al. *Proc. Natl. Acad. Sci USA* 84:7413-7417 (1987); U.S. Pat. No.4,897,355.

For a viral vector comprising a nucleic acid, the composition can comprise a pharmaceutically acceptable carrier such as phosphate buffered saline or saline. The viral vector can be selected according to the target cell, as known in the art. For example, 20 adenoviral vectors, in particular replication-deficient adenoviral vectors, can be utilized to target any of a number of cells, because of its broad host range. Many other viral vectors are available, and their target cells are known.

Throughout this application, various publications are referenced. The disclosures 25 of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

EXAMPLES

Selective elimination of virally infected cells from a cell culture

Rat intestinal cell line-1 cells (RIE-1 cells) were standardly grown in Dulbecco's modified Eagle's medium, high glucose, supplemented with 10% fetal bovine serum. To

begin the experiment, cells persistently infected with reovirus were grown to near confluence, then serum was removed from the growth medium by removing the medium, washing the cells in PBS, and returning to the flask medium not supplemented with serum. Typically, the serum content was reduced to 1% or less. The cells are starved for serum 5 for several days, or as long as about a month, to bring them to quiescence or growth arrest. Media containing 10% serum is then added to the quiescent cells to stimulate growth of the cells. Surviving cells are found to not be persistently infected cells by immunohistochemical techniques used to establish whether cells contain any infectious virus (sensitivity to 1 infectious virus per ml of homogenized cells).

10

Cellular Genomic DNA Isolation

Gene Trap Libraries: The libraries are generated by infecting the RIE-1 cells with a retrovirus vector (U3 gene-trap) at a ratio of less than one retrovirus for every ten cells. When a U3 gene trap retrovirus integrates within an actively transcribed gene, the 15 neomycin resistance gene that the U3 gene trap retrovirus encodes is also transcribed, thus conferring resistance to the cell to the antibiotic neomycin. Cells with gene trap events are able to survive exposure to neomycin while cells without a gene trap event die. The various cells that survive neomycin selection are then propagated as a library of gene trap events. Such libraries can be generated with any retrovirus vector that has the properties 20 of expressing a reporter gene from a transcriptionally active cellular promoter that tags the gene for later identification.

Reovirus selection: Reovirus infection is typically lethal to RIE-1 cells but can result in the development of persistently infected cells. These cells continue to grow while producing infective reovirus particles. For the identification of gene trap events that 25 confer reovirus resistance to cells, the persistently infected cells must be eliminated or they will be scored as false positives. We have found that RIE-1 cells persistently infected with reovirus are very poorly tolerant to serum starvation, passaging and plating at low density. Thus, we have developed protocols for the screening of the RIE-1 gene trap libraries that select against both reovirus sensitive cells and cells that are persistently infected with 30 reovirus.

1. RIE-1 library cells are grown to near confluence and then the serum is removed from the media. The cells are starved for serum for several days to bring them to quiescent or growth arrest.

2. The library cells are infected with reovirus at a titer of greater than ten reovirus per cell and the serum starvation is continued for several more days.
3. The infected cells are passaged, (a process in which they are exposed to serum for three to six hours) and then starved for serum for several more days.
- 5 4. The surviving cells are then allowed to grow in the presence of serum until visible colonies develop at which point they are cloned by limiting dilution.

MEDIA: DULBECCO'S MODIFIED EAGLE'S MEDIUM, HIGH GLUCOSE (DME/HIGH) Hyclone Laboratories cat. no. SH30003.02.

NEOMYCIN: The antibiotic used to select against the cells that did not have a U3 gene 10 trap retrovirus, e.g. GENETICIN, from Sigma. [cat. no. G9516].

RAT INTESTINAL CELL LINE-1 CELLS (RIE-1 CELLS): These cells are from the laboratory of Dr. Ray Dubois (VAMC). They are typically cultured in Dulbecco's Modified Eagle's Medium supplemented with 10% fetal calf serum.

REOVIRUS: Laboratory strains of either serotype 1 or serotype 3 are used. They were 15 originally obtained from the laboratories of Bernard N. Fields (deceased). These viruses have been described in detail.

RETROVIRUS: The U3 gene trap retrovirus used here were developed by Dr. Earl Ruley (VAMC) and the libraries were produced using a general protocol suggested by him.

SERUM: FETAL BOVINE SERUM Hyclone Laboratories cat. no. A-1115-L.

20

Identification Tags for Isolated Nucleic Acids

Genomic sequences, tagged with a vector, such as the U3 gene trap vector, are given a number corresponding to the genomic library of mutant cells from which the 25 sequence was isolated., and a letter indicating a unique member of the library. More than one sequence with the same number and letter indicates multiple, unique sequences obtained from the genome surrounding the vector insert that "tagged" the gene. Such genomic sequences are obtained using vector-based primers, from which sequencing occurs 3' to 5' or 5' to 3'. In the former case, to recover the orientation of the gene into 30 which the vector inserted, the sequence derived from the vector primer must be reversed and complemented. Such reverse complement sequences are designated "rE". In the case of genome sequencing from a primer that occurs 5' to 3' (i.e. the primer is at the 3' end of the vector), no changes are needed, since the derived sequence is the sequence as it appears

in the gene disrupted. Such sequences are designated "B4". Homologies indicated below each genomic sequence are in the positive direction, unless explicitly noted to be on the negative strand. As an example, SEQ ID NO. 27 comprises a nucleic acid sequence encoding a novel polypeptide on the positive strand, while the negative strand encodes

5 ferritin.

SEQ ID NO:	Lab Designation
1	32-3-2#1E/-rE
2	L191B2E#1-RE
10 3	L191B2E#3+-rE
4	21-5-9E-RE
	homology to: emb/AL021154/HS15005 human DNA sequence
5	14A14E-rE
15 6	4cx-b4
7	5a-b4
8	6BSA12-B4
9	X7B/B4
10	x27b4f_1
20 11	12C#A-rE
12	10-3b(5/2/96)/-rE
13	10_4B_4-rE
14	6BE60-rE
	homology to: alpha-trophomyosin
25 15	19D3E-rE
16	L19D16E-rE
17	2b_rE
18	14_24_#6-rE
30 19	7A7'-rE
	homology to: annexin II/dynein I
20	L12cx#6-rE
	homology to: gb:X51760 human zinc finger protein ZFP-36
35 21	L12cx#11-rE

22 19D5E-rE
homology to: 6-pyruvoyl-tetrahydropterin synthase (gb/M77850/RAT6PTH)

23 12_3b#7-rE

5 24 12_3B#8-RE
homology to: gb/AA871174/vq32a08.r1 Barskad bowel MPLRBg Mus musculus cDNA clone 10959265'

25 9B27-2-E
homology to: RAT LOCUS RNU53922 04-MAY-1996; Rattus norvegicus DnaJ-like protein (RDJ1) mRNA, complete Cds, ACCESSION U53922 (on negative strand)

10 26 x15-rE

27 X11-rE
homology to: ferritin H (on the negative strand)

15 28 X20-rE
homology to: LOCUS RATGL5A Rat NICER element (GL5-14)5' long terminal repeat, Acc.No. M59028 M33535N1D

20 29 X4-rE

30 14A7E-rE
homology to: MMSMAD7 3681 bp mRNA ROD 31-JUL-1998 DEFINITION Mus musculus mRNA for Mad-related protein Smad7 ,149 bases

25 31 14A13E-rE

32 14_7#2E-rE
homology to: N-acetylglucosaminyltransferase I

33 12CX#6-rE
30 homology to: gb|AA522204|AA522204 vf98g09_r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone 851872; also 5' similar to gb X51760 zinc finger protein ZFP-36 (HUMAN), gb L20450 Mus musculus DNA-binding protein mRNA, complete cds (MOUSE); Length = 442, 925 bases (shares homology with SEQ ID NO:20)

35 34 12C_2B#9E-rE

35 12CX#11E-rE

36 x5-rE

37 8C5_11-rE

38 191E2E-rE

40 39 19_7AE-rE

40 19_9BE-rE
homology to: LOCUS HS347M6 56583 bp DNA PRI 14-JAN-1998 Human DNA
sequence from PAC 347M6 on chromosome Xq22, CSTF2 (Cleavage Stimulation Factor,
CF-1, Polyadenylation Factor) 64 kD subunit gene

5 41 191E9E-rE
42 191E8E-rE
43 14C_2E/-rE
homology to: gb/H31084/EST104778 Rattus sp. cDNA - 5' end similar to signal
10 recognition particle subunit(19kDa) (on negative strand)

44 14H1E-rE
45 14G3E-rE
46 14G_2E-rE
15 47 6_3_6_2E/-rE
homology to: Rattus norvegicus cis-golgi gp130 (on negative strand); and
a HUMAN EST (on positive strand) AI127398; qb70g11.x1 Soares fetal heart NbHH19W
Homo sapiens cDNA clone (1705508 3' mRNA sequence)

20 48 14H4E/-rE
49 18A_8_4E-rE
50 18A_8_1E-rE
51 SCB2_19E-rE
52 L197B3E-rE
25 53 L195C5E-rE
homology to: H. pylori and C.jeuni

54 21_5_7E-rE
homology to: id3 gene; emb|AL021154|HS150O5 Human DNA sequence from clone
30 150O5; HTGS phase 1 [Homo sapiens]; containing the E2F2 gene for transcription factor
E2F-2 and the ID3 gene for Inhibitor of DNA binding 3 (dominant negative
helix-loop-helix protein), 1R2, Length = 133667, 971 bases

55 L195B1E-rE
35 homology to: vK72b07.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
960181 5'

56 L194c4E-rE
57 L193A1E#A-rE
40 58 L192A3E-rE
59 L1739E-rE

60 L192B3E#13-rE
contains sequence identical to: insulin growth factorII/mannose-6-phosphate receptor

61 3 2 4 rE
5 located in the same region of the genome as calcyclin, but the gene is “read” in the opposite direction
62 36 7 1 a-rE
63 36 5 1 4 a-rE
64 34 25 5a-rE
10 rat satellite DNA (RATRSSID 93 bp, ROD 12-MAR-1984)
65 34 24-126/rE
homology to:
HSU49928 (3096 bp mRNA) PRI 06-APR-1998, Homo sapiens TAK1 binding protein (TAB1) mRNA, complete cds, ACCESSION U49928 NID g1401125, and
HS333H23 (142274 bp DNA) HTG 17-JUL-1998 Human DNA sequence
66 34 23-1/rE
67 36 5 2-6/rE
20 68 36 5 2-196/rE
69 34 23-3/rE
homology to: gb|L16546|RATAP1X Rat P-glycoprotein (mdrlb) gene
70 34 25 23-rE
71 36 5 2-196/rE
25 72 31 3 9/rE
homology to: AA798638 568 bp mRNA EST 10-FEB-1998, vw34b06.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone l245683 5, mRNA sequence, 824 bases.
73 31 3 6-2-rE
30 74 31 3 17-rE
75 31 3 5-rE
homology to: AF046001 2347 bp mRNA PRI 19-FEB-1998, Homo sapiens zinc finger transcription factor (ZNF207) mRNA, complete Cds, 833 bases.
35 76 31 3 15#1/rE
77 24 3 5#1/rE
78 31 4 4#1/rE
79 31 3 19#2/rE
80 31 4 5#1/rE
40 81 24 9 3#2/rE
82 L24 26 1-BL

homology to: AI045472 396 bp mRNA EST 06-JUL-1998, UI-R-C1-jz-h-09-0-UI.s2
UI-R-C1 Rattus norvegicus cDNA clone UI-R-C1-jz-h-09-0-UI 3', mRNA sequence.

83	L24_26_1-B4
5 84	L22_5A1/rE
85	L24_3_2B/rE
86	L24 4-2/rE
87	L24 5-2/rE
88	L24 5-3/rE
10 89	(15-)L28AP/rE
90	L24 26-10/rE
homology to: LOCUS R06687 403 bp mRNA EST 03-APR-1995; yf10a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 126426 5'	
15 91	L24 26-2A/rE
92	L24 26-2B/rE
homology to: gb AA590026 AA590026 vm22g03.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone 990964 , 459 bases, 139A; and Rattus norvegicus Eker rat-associated intracisternal-A particle element	
20	
93	14 7#2E-rE
homology to: N-acetylglucosaminyltransferase I; this sequence shares homology with SEQ ID NO:32.	
25 94	x18
95	31_3_9-rE
96	31_3_6_2-rE
97	31_3_17-rE
98	31_3_15#1-rE
30 99	24_3_5#1-rE
100	31_4_4#1-rE
101	31_3_19#2-rE
102	31_4_5#1-rE
103	24_9_3#2-rE
35 104	14XD#12E-rE
105	70A-rE
106	31-3-4-rE
107	3_6_9-NeoG-rE

108 31_4_2-rE

109 3_2_13-rE
homology to: calcyclin

5 110 3_2_4-E
homology to: pistlre-alpha 1 (with homology to calcyclin on negative strand)

111 L25-10/-rE
homology to: calcyclin

10 112 L24-4-3/-rE

113 L24-9-1-rE
rat id sequence

15 114 17-L25-27#7-rE
homology to: calcyclin

115 L21C1E-rE
homology to: calcyclin

20 116 L24-5-3BE-rE.
homology to:
LOCUS H32572 310 bp mRNA EST 08-SEP-1995 EST107805 Rat PC-12 cells, untreated
Rattus sp cDNA 5' end, ACCESSION H32572, and

25 117 LOCUS AA858747 470 bp mRNA EST 10-MAR-1998 UI-R-A0-bb-e-01-0-UI.s1 UI-R-A0
Rattus norvegicus cDNA clone UI-R-A0-bb-e-01-0-UI, 3' similar to gb|AA473081|AA473081
vd44b07-r1 Barstead MPLRB1 Mus musculus cDNA clone 803413 5' mRNA sequence

30 118 17-3-3B-B4
homology to: LOCUS MMU51002 6495 bp DNA ROD 16-JAN-1997 Mus musculus Dlx-2
gene, complete cds, ACCESSION U51002 NID g1477589

119 L24-26-3/-rE

35 120 12_2B#2-rE
homology to: RNU23776, DNA ROD 10-AUG-1995, Rattus norvegicus Eker rat-associated
intracisternal-A particle element

121 05-17-3-3He-1-T7

40 122 21_5_8E-rE
homology to: emb|AL021154|HS150O5 Human DNA sequence from clone 150O5;
1p36_13-36_22, contains the E2F2 gene for transcription factor E2F-2 and the ID3 gene for
Inhibitor of DNA binding 3(dominant negative helix-loop-helix protein, 1R2, Length =
133667, 971 bases

45 123 X18H-t7

124 18A_8_4E-rE
125 L24-5-2BE-rE
126 L24-4-2AE-rE
127 L24-10-1BE-rE

5

Genes Necessary for Viral Infection

Some of the isolated sequences disclosed here comprise sequence encoding the following proteins: tristetraprolin (human ZFP-36), 6-pyruvoyltetrahydropterin synthase, a eukaryotic DnaJ-like protein, ID3 (inhibitor of DNA binding 3), N-acetylglucosaminyltransferase I (mGAT-1), cleavage stimulation factor (CSTF2), TAK1 binding protein, human zinc transcription factor ZPF207, Dlx2, Smad7 (Mad-related protein), and P-glycoprotein (mdr1b).

Isolation of cellular genes that suppress a malignant phenotype

15 We have utilized a gene-trap method of selecting cell lines that have a transformed phenotype (are potentially tumor cells) from a population of cells (RIE-1 parents) that are not transformed. The parental cell line, RIE-1 cells, does not have the capacity to grow in soft agar or to produce tumors in mice. Following gene-trapping, cells were screened for their capacity to grow in soft agar. These cells were cloned and genomic sequences were obtained
20 5' or 3' of the retrovirus vector, i.e. SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:36 or SEQ ID NO:94; sequences designated with an "x" in the clone name). All of the cell lines behave as if they are tumor cell lines, as they also induce tumors in mice.

25 Of the cell lines, two are associated with the enhanced expression of the prostaglandin synthetase gene II or COX 2. It has been shown that disruption of gene function by retroviral targeting of an upstream gene has lead to increased expression of a downstream gene product, COX 2. When a small molecule inhibitor of COX 2 enzyme was added, reversion of the transformed phenotype occurred. The COX 2 gene has been found to be increased in pre-malignant adenomas in humans and overexpressed in human colon cancer. Inhibitors of COX
30 2 expression also arrests the growth of the tumor. One of the cell lines, x18 (SEQ ID NO:94), has disrupted a gene that is now represented in the EST (dbest) database, but the gene is not known (not present in GenBank).

Each of the genes from which the provided nucleotide sequences is isolated (and all clones designated with an "x") represents a tumor suppressor gene. The mechanism by which the disrupted genes may suppress a transformed phenotype is at present unknown. However, each one represents a tumor suppressor gene that is potentially unique, as none of the 5 genomic sequences correspond to a known gene. The capacity to select quickly tumor suppressor genes may provide unique targets in the process of treating or preventing (potential for diagnostic testing) cancer.

Isolation of entire genomic genes

10 An isolated nucleic acid of this invention (whose sequence is set forth in any of SEQ ID NO:1 through SEQ ID NO:127), or a smaller fragment thereof, is labeled by a detectable label and utilized as a probe to screen a rat genomic library (lambda phage or yeast artificial chromosome vector library) under high stringency conditions, *i.e.*, high salt and high temperatures to create hybridization and wash temperature 5-20°C. Clones are isolated and 15 sequenced by standard Sanger dideoxynucleotide sequencing methods. Once the entire sequence of the new clone is determined, it is aligned with the probe sequence and its orientation relative to the probe sequence determined. A second and third probe is designed using sequences from either end of the combined genomic sequence, respectively. These probes are used to screen the library, isolate new clones, which are sequenced. These 20 sequences are aligned with the previously obtained sequences and new probes designed corresponding to sequences at either end and the entire process repeated until the entire gene is isolated and mapped. When one end of the sequence cannot isolate any new clone, a new library can be screened. The complete sequence includes regulatory regions at the 5' end and a polyadenylation signal at the 3' end.

25

Isolation of cDNAs

An isolated nucleic acid (whose sequence is set forth in any of SEQ ID NO:1 through SEQ ID NO:127), or a smaller fragment thereof, or additional fragments obtained from the genomic library, that contain open reading frames, is labeled by a detectable label and utilized 30 as a probe to screen a portions of the present fragments, to screen a cDNA library. A rat cDNA library obtains rat cDNA; a human cDNA library obtains a human cDNA. Repeated screens can be utilized as described above to obtain the complete coding sequence of the gene

from several clones if necessary. The isolates can then be sequenced to determine the nucleotide sequence by standard means such as dideoxynucleotide sequencing methods.

Serum survival factor isolation and characterization

5 The lack of tolerance to serum starvation is due to the acquired dependence of the persistently infected cells for a serum factor (survival factor) that is present in serum. The serum survival factor for persistently infected cells has a molecular weight between 50 and 100 kD and resists inactivation in low pH (pH2) and chloroform extraction. It is inactivated by boiling for 5 minutes [once fractionated from whole serum (50 to 100 kD fraction)], and
10 in low ionic strength solution [10 to 50 mM].

The factor was isolated from serum by size fraction using centriprep molecular cut-off filters with excluding sizes of 30 and 100 kd (Millipore and Amnicon), and dialysis tubing with a molecular exclusion of 50 kd. Polyacrylamide gel electrophoresis and silver staining was used to determine that all of the resulting material was between 50 and 100 kd,
15 confirming the validity of the initial isolation. Further purification was performed on using ion exchange chromatography, and heparin sulfate adsorption columns, followed by HPLC. Activity was determined following adjusting the pH of the serum fraction (30 to 100 kd fraction) to different pH conditions using HCl and readjusting the pH to pH 7.4 prior to assessment of biologic activity. Low ionic strength sensitivity was determined by dialyzing
20 the fraction containing activity into low ionic strength solution for various lengths of time and readjusting ionic strength to physiologic conditions prior to determining biologic activity by dialyzing the fraction against the media. The biologic activity was maintained in the aqueous solution following chloroform extraction, indicating the factor is not a lipid. The biologic activity was lost after the 30 to 100 kd fraction was placed in a 100°C water bath for 5
25 minutes.

Isolated nucleic acids

Tagged genomic DNAS isolated were sequenced by standard methods using Sanger dideoxynucleotide sequencing. The sequences were run through computer databanks in a
30 homology search. These genes can be therapy targets particularly because disruption of one or both alleles results in a viable cell.

What is claimed:

1. An isolated nucleic acid comprising a nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, and SEQ ID NO:127.
2. A nucleic acid comprising at least 20 consecutive nucleotides of a nucleotide sequence of claim 1.
3. A nucleic acid comprising at least 30 consecutive nucleotides of a nucleotide sequence of claim 1.
4. A nucleic acid comprising at least 40 consecutive nucleotides of a nucleotide sequence of claim 1.
5. An isolated nucleic acid encoding the protein encoded by the gene comprising the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5,

SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, and SEQ ID NO:127, or a homolog thereof.

6. A host cell containing the nucleic acid of claim 1 or 5.
7. A nucleic acid comprising a nucleic acid that selectively hybridizes under stringent conditions with the nucleic acid of claim 1 or 5.
8. A nucleic acid having a region within an exon wherein the region has at least 50 % homology with a nucleic acid of claim 1 or 5.
9. A nucleic acid having a region within an exon wherein the region has at least 60 % homology with a nucleic acid of claim 1 or 5.
10. A nucleic acid having a region within an exon wherein the region has at least 70 % homology with a nucleic acid of claim 1 or 5.

11. A nucleic acid having a region within an exon wherein the region has at least 80 % homology with a nucleic acid of claim 1 or 5.
12. A nucleic acid having a region within an exon wherein the region has at least 90 % homology with a nucleic acid of claim 1 or 5.
13. A nucleic acid having a region within an exon wherein the region has at least 95 % homology with a nucleic acid of claim 1 or 5.
14. A polypeptide comprising the amino acid sequence encoded by the nucleic acid of claims 1 or 5.
15. A nucleic acid comprising a regulatory region of a gene comprising the nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, and SEQ ID NO:127, or a homolog thereof.

16. A construct comprising a regulatory region of claim 15, wherein the regulatory region is functionally linked to a reporter gene.

17. A method of reducing or inhibiting a viral infection in a subject, comprising administering to the subject an amount of a composition that inhibits expression or functioning of a gene product encoded by a gene comprising the nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, or SEQ ID NO:127 or a homolog thereof, thereby treating the viral infection.

18. The method of claim 17, wherein the gene is selected from a nucleic acid encoding a gene product from the group consisting of, or the gene product is selected from the group

consisting of: tristetraprolin (human ZFP-36), 6-pyruvoyltetrahydropterin synthase, a eukaryotic DnaJ-like protein, ID3 (inhibitor of DNA binding 3), N-acetylglucosaminyltransferase I (mGAT-1), cleavage stimulation factor (CSTF2), TAK1 binding protein, human zinc transcription factor ZPF207, Dlx2, Smad7 (Mad-related protein), and P-glycoprotein (mdr1b).

19. The method of claim 17, wherein the subject is a human.

20. A method of reducing or inhibiting a viral infection in a subject comprising mutating *ex vivo* in a selected cell an endogenous gene comprising the nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, or SEQ ID NO:127 or a homolog thereof, to a mutated gene

incapable of producing a functional gene product of the gene or to a mutated gene producing a reduced amount of a functional gene product of the gene, and placing the cell in the subject, thereby reducing viral infection of cells in the subject.

21. The method of claim 20, wherein the cell is a hematopoietic cell.
22. The method of claim 20, wherein the subject is a human.
23. The method of claim 20, wherein the cell is from the subject.
24. A method of screening a compound for effectiveness in treating or preventing a viral infection, comprising administering the compound to a cell containing a cellular gene comprising the nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117,

SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, or SEQ ID NO:127, or a homolog thereof, and functionally encoding a gene product necessary for reproduction of the virus in the cell but not necessary for survival of the cell and detecting the level and/or activity of the gene product produced, a decrease or elimination of the gene product and/or gene product activity indicating a compound effective for treating or preventing the viral infection.

25. A method of screening a compound for reducing or inhibiting a viral infection, comprising administering the compound to a cell containing the construct of claim 16 and detecting the level of the reporter gene product produced, a decrease or elimination of the reporter gene product indicating a compound for reducing or inhibiting the viral infection.

26. A method of screening a compound for effectiveness in treating or preventing a viral infection comprising contacting the compound with the gene product of a cellular gene comprising nucleic acid set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID

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27. A method of suppressing a malignant phenotype in a cell in a subject, comprising administering to the subject an amount of a composition that inhibits expression or functioning of a gene product encoded by a gene comprising the nucleic acid set forth in SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:36 or SEQ ID NO:94, or a homolog thereof, thereby suppressing a malignant phenotype.

28. A method of screening a compound for effectiveness in treating a viral infection, comprising administering the compound to a cell containing a cellular gene functionally encoding a gene product whose overexpression inhibits reproduction of the virus but does not prevent survival of the cell and detecting the level of the gene product produced, an increase in the gene product indicating a compound effective for treating the viral infection.

29. A method of screening for a compound that can suppress a malignant phenotype in a cell comprising administering the compound to a cell containing a nucleic acid functionally encoding a gene product encoded by a gene comprising the nucleic acid set forth in SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:36 or SEQ ID NO:94, or a homolog thereof, and detecting the level of the gene product produced, an increase in the gene product indicating a compound effective for suppressing the malignant phenotype.

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Page 1 of 4DECLARATION AND POWER OF ATTORNEY
FOR PATENT APPLICATION Original Supplemental Substitute PCT

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am an original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled "**MAMMALIAN GENES INVOLVED IN VIRAL INFECTION AND TUMOR SUPPRESSION**", which is described and claimed in the specification

(check one) which is attached hereto, or
 in International Application No. PCT/US98/21276, filed October 8, 1998,
and as amended on (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information known by me to be material to the patentability of the claims of this application in accordance with Title 37, Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119 (a) - (d) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate relating to this subject matter having a filing date before that of the application on which priority is claimed:

PRIOR FOREIGN APPLICATIONS: (ENTER BELOW IF APPLICABLE)			PRIORITY CLAIMED (MARK APPROPRIATE BOX BELOW)	
APP. NUMBER	COUNTRY	DAY/MONTH/YEAR FILED	YES	NO
PCT/US98/21276	International	08/10/98	X	

I hereby claim the benefit under Title 35, United States Code, § 119(e) of any United States

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provisional application(s) listed below.

APPLICATION NUMBER	FILING DATE
60/062,021	October 10, 1997

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose all information known by me to be material to the patentability of the claims of this application as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

APPLICATION SERIAL NO.	FILING DATE	STATUS (MARK APPROPRIATE COLUMN BELOW)		
		PATENTED	PENDING	ABANDONED

I hereby appoint the following attorneys and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

1-00
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3-00

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 Organ, Edward L.
 DuBois, Raymond N.

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nnacangngg	atgtgtgtt	cttttttcag	cagtgggtga	ccggattct	aagaccctta	300
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cgcagctggg	ngtgggtgt	tgtaccttta	atctcagcac	tgaggaggca	cngatatctc	780
catctctgt	acttccagac	cggcncgtcc	agagcaagtt	ccaggccacc	cagatgagat	840
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<210> 4

<211> 974

<212> DNA

<213> Rattus norvegicus

<400> 4

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nttattggcc	ncnnttcccc	cccgctntt	cncnccctt	cttngagant	ngtgnthcna	180
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accggtnntgg	gttngnanc	nnctgnanc	nccnattttgg	gttccggntt	accnngggtt	300
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acngntcna	ccttatttgc	aattaatttt	tccttngnna	ntctgncccc	cnngnattt	420
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cacagactgc	aaagtgtgc	gagggaggg	ggctgtgca	aaaaaaaaaa	aaaaaaaaaa	840
aaaaaaaaaa	ccgaggacgc	agaagtttgc	ctgctgaccc	atttggtgc	tgtgtgc	900
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<210> 5

<211> 850

<212> DNA

<213> Rattus norvegicus

<400> 5

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gttaggggg	cccgngggaa	aattttaaaa	ccnngngggc	tttttgc	taagggaaaa	180
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ggantaacag	ngnttgc	gtntngcnaa	acgaagagtn	tcctgnttgg	aataggngtt	360
cngttc	gancagatt	tangngtgg	agnaaggatt	ngcagataa	angcngt	420
natgnancnt	ggancaggtc	nggnccnagn	ntacagatga	tgnnccana	canganataa	480
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ngccttnana	antgnctaga	gaaccancag	tggntanggg	ntgcccnnnn	naccaggaa	600
gaccggggc	gtgnccgata	ttgacacanc	agatnnccatt	tggggncggt	tcgagggtt	660
atgntc	actacnagan	angatntcc	aaccggaaat	ncggtgctcc	ngtgcgtcc	720
tgnaatgat	cgnccggnaa	cctcatatcc	aagaaacnat	acagcagtgg	nntccgagtc	780
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<210> 6

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<211> 531
 <212> DNA
 <213> Rattus norvegicus

<400> 6

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ananacatca	gagatctcn	gnacagtgtt	tcacaagagt	ctatcncana	gagcacatct	180
gccccggng	anacacaact	ctaaatgtgt	ctcanntgat	ctctctnttg	tgtctctnac	240
atatngggac	atgctctcag	agtatnggnt	cttttngncn	cttnngcaca	cacacacaca	300
cacacacaca	cacacacaca	cacncttctc	tctggcacag	ggntatggca	nagcacatnt	360
tnngagntca	nagctntata	tgagtggtg	gcgaaagagng	tnatnanann	gacnnccca	420
gcnnatata	gggggnngnnc	tctngggctc	tcttnggnna	tntngggng	agtctgcnca	480
cacaggcgct	cnnacccanc	nnnttggggc	cccccagng	ttttcnccc	c	531

<210> 7
 <211> 572
 <212> DNA
 <213> Rattus norvegicus

<400> 7

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gngacangt	agnncncccc	atnttcnccc	cccttca	ctgccccnag	agagagaaaan	480
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<210> 8
 <211> 906
 <212> DNA
 <213> Rattus norvegicus

<400> 8

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agagcccccc	agaaanccc	tntctcaan	aaagagaaaag	agaagancg	gnagnagaga	180
ganaganaga	gagagagtgt	gganctnt	cctcnganc	ccannnanan	ngtngggcnc	240
actctcnngt	gnngngnacc	ccnngggatt	tncgctgtc	cccttngct	tgtntanga	300
ganananatg	tntagtctt	ctntcgcccc	ctccgntgtc	acgtgtgcgg	ggcccnngag	360
acacagacac	ntctctcang	ggaaacacat	anngactcnc	acntgtgttt	atattcnccc	420
ctccnctca	cacanacaca	cacacagnag	atattnnct	actctctc	tgtcacaggg	480
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ctctcngaga	angngaggc	gnnttacntt	cccnngtggcg	tgtncngcc	cccgagactc	600
cccttngnac	ccccctntna	accctctntt	tgaacncaac	ncacntccc	cnttttctcg	660
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<210> 9
 <211> 914
 <212> DNA
 <213> Rattus norvegicus

<400> 9

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gactcccatc	tctntntn	ccccaganc	tggngaacgg	ngtggngna	nccntntctg	120
ttctcnantc	tctaaaagng	cnaaaagcgc	ananacacgn	gcctcttat	anatctcagc	180

tgtcccnngn	nctctcngac	ccctnntctg	tntgagagac	accctntctc	aaaatatagt	240
gtacacgngc	tttgnggctc	tcccctttc	tctccactnt	tgagngngaa	acgcggngtt	300
ntctctgaga	tgtaganagn	gtcccctnct	cnatataatgt	gttncccact	ccnnagggng	360
tctcataaaa	atcnctntc	tcaacaccac	cnccctcnacc	cccncacga	gaacacnctn	420
ccaccnchn	gacacaaana	naaggngtnn	anaacccan	aaaaactnng	ntntcngntt	480
tacacacaca	cacacnca	ctcnncaca	ccccacnna	aatggagaa	aaaacagaga	540
ggngtgggt	tttgnntcaa	cacntntt	cctctgtgt	gnnataatc	aaaatatttc	600
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anangagaag	gnccaaaaag	gnnggngtct	tcteggaat	ncncctttt	ggccccccaa	780
cctgggttt	tttccccc	ccttttaatn	anttttcna	nacaaanctt	tnngngtttn	840
ggaaaangcc	ttttnctgn	nntttttcc	cttcccctt	tnnanggnt	ccccccccc	900
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<210> 10

<211> 400

<212> DNA

<213> Rattus norvegicus

<400> 10

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acagttat	aatattt	cataattt	cac	aagactttat	attgttataa	120
gtgagatata	tgtgatt	ctgtgtgtt	ctcagaggg	gttgggtt	ttggggataa	180
tagttgccc	ctcgccgggt	ctatattt	atatgtgaca	caatataat	gagagat	240
tggtatata	tatttcc	cgcgggggt	gagatttac	acagggggag	agttttccc	300
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<210> 11

<211> 880

<212> DNA

<213> Rattus norvegicus

<400> 11

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cgaatttta	aaaaccgtcg	ttagaggaa	tgaagg	gccgaccatt	acctganagt	180
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tgttcagtc	cacattaagg	ttgc	aatt	tgca	tgataacaag	420
ctttcnac	acaatataa	gtnt	cc	taagccatgg	gagacaatt	480
tccaccacag	gtctgc	cac	tataatc	ttct	cattctgttt	540
ggagaaaaatt	ccagtcc	ggtc	gat	tc	tc	600
gctcattcct	hacatgggt	gat	gg	atctgagg	ggcagtg	660
gtaagcttga	tttgatttcc	actgt	gg	gg	aaagaaac	720
ccatctctct	ctctaa	cc	actt	ttt	ttt	780
agcagagat	agctcca	aaat	ttt	cc	cc	840
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<210> 12

<211> 909

<212> DNA

<213> Rattus norvegicus

<400> 12

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agcnnaaanc	gaggagg	ganggang	nngnngn	gaaggcgc	aagnnggtcg	240
ngagcgg	nggnnaa	tgggaac	gacagacgg	ccnn	gcangng	300
gagnncg	agngag	gn	gac	ng	ng	360
gaggnncg	gacggn	nnnaga	gac	nn	nn	420
cangagt	gnngagn	acaggccc	gcnc	cc	cc	480

gggtgggngg	ggcncggaga	naagaccaga	ggnnngaggg	cganggcng	ggtnngcccg	540
ggcccccna	aaaaaanncc	aaaaaaaan	aaggggcgn	gcngggcng	ggaggagcgc	600
tnnncgtang	tngantgacg	gaggcngna	atngggcgn	gccanncnag	ggcgnagagg	660
cccaagngcg	gnaggnngaa	gnanagancc	ngnnggtng	gagnganagn	gcnnngnncc	720
naccnccngn	gttganggn	cccacgncgg	ngcaggcgn	nnaaagngag	tcccnaaaa	780
nntcnggtn	tnacancgnc	cggggnncgc	cgcngngtcc	cgncacacng	gannncggag	840
anngctnnt	ntctncacan	ggngccanac	nngntgctat	gcaaaaagggg	cgnacttcna	900
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<210> 13

<211> 927

<212> DNA

<213> Rattus norvegicus

<400> 13

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tttnaaaaag	ggcgncnat	ataaaangacn	ttcgggggg	tttgaanagg	gcccgaancn	180
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gngtggaaaa	acanggataa	acggaaan	ggggttat	nggtagnaa	ttgnntccag	360
ngngnccagg	aaattggcct	gtccaaaatt	cttttccng	ctttaagac	aggcaggtat	420
tatttggcag	caggttatta	cnataggnaa	gtaaataaca	atgggttaagt	gcctggcaca	480
ggccagggt	agtagggcat	gtatggat	ttaaacatta	cccttcattcc	tgagaaaanaa	540
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tggtaacagt	taagccaa	ntatgantca	caaggacga	catggcagg	ntagggtaca	660
gaatcagtgn	tcagagactc	caggggcacc	cctgatttcc	tttgcgtca	cacagacact	720
gctccaggg	caaccctcc	gatgtgat	tatgacttcc	tgatggtgac	gctgcccgtga	780
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cagagcacag	tggcaangac	tttcatttct	nttgnctt	cccaggggc	gtnccaa	900
						927

<210> 14

<211> 848

<212> DNA

<213> Rattus norvegicus

<400> 14

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tnattnaan	gggngttagt	tctgttnggt	tcattcc	aaaaaaaac	aaaacaaaac	180
aaacccnagc	ttctgcatt	gccaccngt	gnggcacca	cccttnangc	attgccc	240
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ttccatgtcc	ttgcacttct	gcttccactt	cntgttgc	gacgagctgt	atgnntcagaa	360
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gtaaatgttc	atgcaccct	cctgttgc	ccctcacnt	catgttgc	tgatgac	480
accgtggctc	ccccannann	aaaanancatc	catgttgc	ccttttgc	gctttcttgc	540
ataacctagg	ataggttac	ttttccacgt	tgcaactaaca	agggcacgc	cattcggtcc	600
gtgaaaccac	ctcggcatcc	ttttatntca	tagaggcaaa	tntagttgt	ttctgcccag	660
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						848

<210> 15

<211> 896

<212> DNA

<213> Rattus norvegicus

<400> 15

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nggnngnnaaa	gagnnann	tttcaagggt	ccgnaacaa	aagttgagng	angattccna	180
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gggagttaaa	aagagtccacc	aaatagggaa	aaaaagttng	ggggaggggnn	aacnacnnggg	300
taaaggttcc	aggaccagag	ngttcagnac	caagtttcag	tattcaggag	gacagagttc	360
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gatgtcaact	ccaggcagta	ggggcgcac	ggcattgtg	ttnttagagag	anttccccag	720
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agacctattt	cttccgaga	ggatcggacc	aaacagcaga	ttntgctcaa	ggcccttcaa	840
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<210> 16

<211> 858

<212> DNA

<213> Rattus norvegicus

<400> 16

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tc当地cnctt	tgacattatga	gggttgataa	cngctgttt	tngattttgg	ttaacanggg	180
ngggngcntt	tttnggniga	cctntagtn	ntc当地ngccg	ggcattttgg	ntacctttt	240
attttngaa	gtncaggat	gttggtaact	ggaatattt	cttagaagtg	accatgattt	300
tatattttat	taaatatata	cttagattca	ntctttgcct	aaggcctggat	gttgggtggtn	360
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acacagagaa	gaatnacaaa	caaacaaca	aaatatttctn	gacagaaaca	antaaatata	540
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<210> 17

<211> 551

<212> DNA

<213> Rattus norvegicus

<400> 17

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gngatctntc	tctctgtgca	cgaganattt	tagaggggga	tatccccggg	gtgtngccng	180
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gaggganana	cattttntg	tggggccccc	ccacaananc	acnaacaana	tatttcag	300
aancncatgn	ganaatcggg	gggggggggg	ccngtgnna	cacnatancc	ngggngatna	360
nanagacacn	nnatatntct	gggntgtgna	aanataanac	aagancanac	atgnggagan	420
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<210> 18

<211> 888

<212> DNA

<213> Rattus norvegicus

<400> 18

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gaggggccaa	aaggataagg	aggatgattt	attgggttgg	gaggcgtact	tggaaagagt	180
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acaattcaca	agatttttcc	acagggagtt	ctaggaggtg	gtcccattag	ccggtagggg	360
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aggccttaaa	cttgcgtatcc	tcctgtctca	gcctccctagg	tgttaagatg	acccaaatgt	780
aaaccatgtc	cagttacttc	ctcctaattcc	catcttcaga	tatcctttaa	gaccaaattha	840
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<210> 19

<211> 867

<212> DNA

<213> Rattus norvegicus

<400> 19

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tggggAACAA	aaaaaaaattt	ttaaaaattt	ccaggggggt	tttgaaggca	ggtgatttaa	180
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<210> 20

<211> 897

<212> DNA

<213> Rattus norvegicus

<400> 20

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cggctaccgc	tgaggtctta	gccactca	agacccagcg	gcagtttctg	aataacttcc	840
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<210> 21

<211> 435

<212> DNA

<213> Rattus norvegicus

<400> 21

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ncaagctaga aaggt				435

<210> 22
 <211> 894
 <212> DNA
 <213> *Rattus norvegicus*

<400> 22

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atgttaggcag ctttgaaggg	atttntcctg	agaggatctt	ccggatcaga	gtatatcgcc	420
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gcagtgcggt gacacacgtg	ggcacacccc	acctgtgcag	ccggggctc	gcgntgaagg	600
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ttgnttaggct ataagtgaaa	gaccacan	gtaggtttgg	caagctagcn	aaag	894

<210> 23
 <211> 594
 <212> DNA
 <213> *Rattus norvegicus*

<400> 23

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nagagtaatt tcaaaagccc	cagnnttgg	gaatcantt	ttgaanataat	gaaaaggccc	180
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<210> 24
 <211> 586
 <212> DNA
 <213> *Rattus norvegicus*

<400> 24

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tccaaataga tgtatttcaa	aagccccagc	tttggatc	agttttgca	ntatatgaaa	180
aaggccttan tgnttcggga	ttattaaggc	ccgctgagga	cactgttgg	gcgcntcaag	240
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ctgtttatct ataaaatctt	tcaagcagat	cttgcagcca	actaggtaca	agagtcggat	360
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aactccacnt tcaaggtatc	cgctccgggt	tagcagcccc	ccaaacgcccc	tgctggnttc	540
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<210> 25
 <211> 909
 <212> DNA
 <213> *Rattus norvegicus*

<400> 25

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gggnnnnagc	cgattaaaag	aaggngggag	cagnagggga	agccgagctt	cggccgttt	180
ccgnaccctt	aaccctgttt	gttcgggggg	ggagngtgc	accnaccgg	gnngngtgc	240
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ccggcattcc	cggcaccc	ngaagacnga	gcccgggtca	ggacnnaca	ntccccccca	360
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gtcacttgcc	ggaagtccc	ccntcgttt	ctgcccaccc	ccntcgtta	cctggcaac	660
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<210> 26

<211> 576

<212> DNA

<213> Rattus norvegicus

<400> 26

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tccccactct	acatctgtt	tcggagcacc	cccccacca	gagggcgctg	tcagtcata	180
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tttcagagaa	ttctctaata	ctcgggtac	ttccgcccc	ctgtcaagac	ttcacatatg	300
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<210> 27

<211> 853

<212> DNA

<213> Rattus norvegicus

<400> 27

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tccttgaan	acccngaaaa	attcatttnc	agaggggtt	gaagggggag	ccgaaaagaa	180
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<210> 28

<211> 825

<212> DNA

<213> Rattus norvegicus

<400> 28

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-10-

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tgaaagggn	tttatcgcaa	nacnccgggg	gggggttttt	ttgaaagaga	agggaaaaag	180
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acttcatcat	gtgaatagcc	aatcatatgt	gaacatgtnt	atgtgttcg	tttgaatcca	600
ccaatccc	taantatgt	ntgttctgna	cgc	tgttcccca	tccntataaa	660
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<210> 29

<211> 861

<212> DNA

<213> Rattus norvegicus

<400> 29

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cccnagnan	naaaattttag	tcagtn	gnaaccgac	nananaggaa	caggtttccc	180
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ccctnacn	atgnancaga	gagagagagn	accgtatant	nantgnaaga	gagg	840
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<210> 30

<211> 149

<212> DNA

<213> Rattus norvegicus

<400> 30

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<210> 31

<211> 857

<212> DNA

<213> Rattus norvegicus

<400> 31

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acggaaa	agn	agacngt	aa	tgna	240
atcng	ca	accaccgg	ttt	tg	300
aaggattt	ca	ggagatc	ttt	cg	360
ggagcgg	na	accattn	tcgg	g	420
angtcgt	gggattt	tttt	actat	ttt	480
ttnn	tcagcccc	ttc	ccctt	ttt	540
acgg	ngcacc	ttt	taggcac	ttt	600
gnat	atcg	ttt	ctgcgc	ttt	660
aaanact	gatc	ttt	ttctgt	tt	720
			gac		
			ccat		

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<210> 32

<211> 1630

<212> DNA

<213> *Rattus norvegicus*

<400> 32

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<210> 33

<211> 883

<212> DNA

<212> DNA

<400> 33

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gtcttcata	gacctgccaa	tcagaagga	aggcgggctt	ttccgggtc	ntaggtgtag	600
gattcgctca	gtatgttta	agtcttaact	ggtntggct	gctgtgc	ctgtcctgccc	660
gttggattn	ntgaggcatg	ttcaggcaag	ctccaaagtt	gcgacatgt	gagcacagg	720
cgagggggg	cggcggacg	ggcaggggac	tgagcagtgg	gagctgggt	gggggtctt	780
tcccggttct	gagttggaa	ccgcggctac	ccgtgagg	ttagccactc	actagaccca	840
gcggcagttt	ctgaaataact	ttccattgt	qqgctqcaac	tct		883

<210> 34

<211> 913

<212> DNA

<213> Rattus norvegicus

<400> 34

ttccccccna	aaaaaatatt	tttngggacc	canaaaaaan	ggtccnggn	cctgtttct	60
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ggtttntcc	naggggggga	gaccctttn	nccgcgggccc	tttcgnaatt	ttttggtcca	180
ccngtnaaag	atttcccat	ggcgcacca	gtacgggttg	cgagggngtat	taggcggnaa	240
cggttttta	gtgggcctaa	tacggnnat	aggaggacga	tttgcgttgg	tttgtnagac	300
cagtacctt	gnaaagagg	gtatgttga	tccggcaacc	aaccacngtt	gtagcgnnggt	360
ttttgttga	agcagcanta	acgcgcagaa	aaaaggatnt	caggagatcc	tttgatttt	420
cttcgggttc	ngacgtttag	ttgtgtggat	tgtgagcgg	taacaatttc	acacagattc	480
cgatngtagt	ccaatttgg	aaagacagga	tatntttccc	ttcaaaagaaa	acagaaaaat	540
acagaaacgt	taattttca	atctcnaatc	tttcnttctc	tcttcnntca	ttcattcatt	600
cnttcttct	tctttcttcc	tntcttctn	nagaggaggc	atgcttagggt	aacagttagct	660
cattttaaaa	tctggcacct	ggaattaatt	tagggacaaa	acacctttat	gcaaaaaaaaa	720
gttatgttt	ttccatggaa	cacagaaaa	tcaaaattaa	aagaatataa	caaaggcttt	780
ggtgattttgg	taggattttt	ttttcctgg	agggaaaaac	agatgacttg	gaaagtgtta	840
ggaacatatac	aagccccagg	gaaagaaaaa	cgtttgattt	gtattaatta	aaacactgct	900
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<210> 35

<211> 320

<212> DNA

<213> Rattus norvegicus

<400> 35

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ggttggtaa	atgaagagga	gagacagagt	gggaagtcgg	cttagtggat	atggacttca	120
aatttgcata	acaagcaatt	caaatgat	tcgtggcgtt	gactggat	aagaccgtt	180
tgcaaaagcag	tgntcataag	agagaaaaaga	gagagagaga	gagagagaga	gagagagaga	240
gagaagaga	gagagtgtt	gttgcgtt	ttgtgtgtt	tgttattgg	tttataacaa	300
gatntacntt	tggtaactt					320

<210> 36

<211> 389

<212> DNA

<213> Rattus norvegicus

<400> 36

ggggggggngc	naaaagggtc	tttcttttta	naaaaatcnn	ggangggaggc	cncnanacgg	60
ctnttanann	tnttcnggggt	gtncctcncc	gntgtggga	atganatntc	gntctcgaca	120
tcaggggatt	ggagattttc	tgnctcncc	nctcacinacc	cagaagaagc	gcacagagan	180
cagatcata	catcatcac	accttnttcag	ctacagagcg	antntctan	aaggggactc	240
ggggganaac	acaaccctcc	tccttctctg	actgngagng	ccgcntgttag	gntctgtcta	300
ccancaagn	cttgcagn	ntngaaactt	ctctntgggg	tagagtgtt	tgnnggagca	360
gggcgtantg	ttccaggnc	agnctttca				389

<210> 37

<211> 882

<212> DNA

<213> Rattus norvegicus

<400> 37

agnaacgcgg	ncggnggnnc	tcnccnngcg	gagcnggncc	nccccnnngn	ncccagaana	60
gnagcgctcg	nganannnc	acgngnagac	nnngctgccc	ccncgngncc	anggcntnn	120
nccnnccccc	cgnatccgn	ncnccccc	ctccctnggg	gnnggggggt	ccngngccg	180
ngngnatacc	nggcganncn	ttgtggccccc	gnnggggggg	naggacccccc	ggcaccggcc	240
cngacccana	ncagnngctt	ngtggggggc	ccccccgc	nagaacgaat	tncgcncnc	300
gcccgccgca	tcggaacncn	cctagcagng	cgtcntgcta	ggcnggnnn	cgggnatccg	360
caancccncc	cttngtaccc	ggacagccgn	gggnccgtat	gggtgtngcg	ntngccgt	420
gccanntncc	tttngaaang	acncggnagc	tnttcatccg	cctcacaaac	cncngggncn	480
nggggggctn	tntcntngnc	cgccccccgc	gtngcgc	aaaaaaa	aannccggcn	540
tccnccctc	ttttggccng	ggtnccccgc	ncaccccg	ccgagtnccn	nnccccccac	600
aacctcacac	cgatccnngt	gggtccnn	ngggagtgc	ncngcnnag	cngnnttctc	660

-13-

cccatnnncgc gnngcttnag cgngccnnnn cacngttgt nnngnnntgc ctcccctcn	720
tccttgaggg aaaagcccg aacngntctg tggaccacnn tgctgaggg ctgggcggcn	780
cgntctctct ctctctcnct ctctctctct ctctatctct ctttctctct ctggggcccc	840
tcccttngnt nngccanaag nnngcnhacc cgtaaagtaa gt	882

<210> 38
 <211> 975
 <212> DNA
 <213> *Rattus norvegicus*

<400> 38	
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tttagcnggg ttctcnagtt natgtaacc nagtacttaa ttgcnncnct tgataaatgc	120
tngatcctna naatttcaac aaccgcagga ccattttga acttggcggn ngtttaccct	180
tnatgnnctt tccnnnaaaat ggcttcctt gncatcnaat agtgnlgccc ctaaccctn	240
ggttccggag gatgcattng tggntgtng tttgnccctt agcatgcngt tccgtnacgg	300
gancaagntt ntcaatgttc cntcacncca tacttngct tgggtacaa nttgtatatc	360
ttcgggattt tatnagtta tgcgtnttt tcataaaatc acttggat ttggcttaa	420
ngttaggaca acttnccaca gtttcttgg a tcccnctaa catgttaacg ccattttgtt	480
cttgataact aaagtgcacat gtcnntntng acactaacaa tcacaaatg ggagtagccaa	540
tcaacttga gaaaatttaa aagatgccc atctcttgc tcagcaagta ttcagccagg	600
atttatttct ttatgtaaaa attagcaac atttctatnt cattcacgtg caaattttct	660
ttgattgtta attaagattt aagtgtatg tattggccaa ataagtctca ctttaaaaaaa	720
tattttttt tgaatttata tccatgaatg tttgatctgt atagctattt tatataagta	780
tatgcaagga ttgctaaaac aattttttag g taaaaaaga tccttaggtt aatgttta	840
agactctcta taccgtcatt aaaaactctt caccagcatt tactatgtt ggactttcag	900
agactctcaat caacttttc ccacccagtc tactgaaagn ttccacctgt a cggcccaa	960
gcaactgag atntt	975

<210> 39
 <211> 850
 <212> DNA
 <213> *Rattus norvegicus*

<400> 39	
ggggaaaccc acggtnaagg gnngganaac naggtanctn tttctccggg ttccaanaat	60
ngaangcctt ccngaggggcc ngaaaancat tnctcnnga gccgttcaag ccagnagggt	120
ggttcaaaac aatgtttaag ttgtggggag aacnagnacg tccgttcceng acccngtta	180
tcntaaagga gacggnggtt aaaggttagg gggtnngaca gtcctgtgg tttcaagga	240
ggaggagaca agttgnatc caggnngnc a gaaanacctg ttaattctt gaccnacccg	300
atgnntggag agcnaaggcg gattttccg gcaagtggcc gatttcaacc caggtcccg	360
ccngttttc ttgtttaggc aaggccctt tagtccngna ggacgcccct tggggccag	420
ggtatcacgg cccccctnng gtttccattt gcaagtggta ttggaccatg gatcaactgt	480
tcctntgcc ggaagttcca gatttccaaac tttgngantc ccatntgca cttccatgtt	540
tgccngtggg acttttnta atatcttgc acccgcttcc catttcccca cccccntgnt	600
ccctcggga ggaatcaccc cccagtgtgt cacttccgtt aggnacttcc aaggntagat	660
gagtgtggg caggcctcac nttggcccag ttantcaatg cccacagat agtttttg	720
agacngtagt aaggctttag gggaaaggat gtatgcata ctttccttgc tggccctca	780
gcactgtgag tagacccac acatcaggc tgcgttgc gatctctgg gagggttga	840
agttcgagg	850

<210> 40
 <211> 889
 <212> DNA
 <213> *Rattus norvegicus*

<400> 40	
ggggtttcca aaaatttggg gnttggana aaccttcggg gaataaaaaca acngnnnaaa	60
attaaggggg gccgggggaa aaaggagatt nattaaancn ccacccgaat tnaaacnccc	120
nccgggaccg naaccgttt tggcnaaan ncgagaagtg cttccnggc aaagttaggg	180
accaaaggtn gggggagaga attggggttt gtncaatg cccgttccnac ggaaggagcc	240
ggttggggat ttttttca aggagngnt tttgngaccgg agcacctcng gggngaccat	300
ggggnttggcc ttttagagac cngcngatg ttttgggtc gnattcgggg agggatttcg	360
ggggcctcag acnggggagg agtccctgc gttcccnatg ggaccgggtt tcggccgggt	420

-14-

gcagtttcgc	tgctgtcctt	tggcaatgng	cntgggnatt	ngtgggcaga	ngagattccc	480
cngcccccgc	natttcccn	gttccagttc	ntaggnacca	gaggtttcc	gcagtgat	540
tcaaggagnt	agantntagc	gtctgtntn	tntgcgttt	ccccttcatg	attctcagtt	600
attttttagg	agaaaaggtg	cgtggaaaca	gagcgtccct	gttccgtgct	gtttctcnta	660
gccccaaaata	cagatttaat	tctgaagcca	tcgaccccc	tatccacttc	ccgcccctc	720
ataaacgtgt	aatatggctt	gcttttctt	tgtaacgttt	catccaacca	tagtggtagc	780
ggccacctgg	catcttgagg	tgggttgcga	atgagtgaat	gaatgagtga	gtgaatgaat	840
gaatgaatga	atgaatgaag	caagcttcag	ggagatttc	agagaagtg		889

<210> 41

<211> 929

<212> DNA

<213> Rattus norvegicus

<400> 41

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ttccaaatcg	gtttaantgg	nccnccgaa	ncntnttt	tttggcagaa	ggtgaanttc	180
nttggggccc	ttgtttaagg	gtttttagcc	ttaaatttgt	tgntnagnnt	ctccntaatt	240
agttcattcc	tttgaccatc	tttgnccct	ccatcttgta	aacanttaag	tctattgcat	300
tccactttnc	tntcagttnc	cgtttnaccc	tcctnagcag	aaccgnttc	tcagctntgg	360
atgttccaa	anggtttccc	aacctatgct	caataccaca	ggcagcttc	aggagggaga	420
antggatgt	attdaacagc	attttgaccc	aaacttttag	gagcagagag	gactttaccc	480
aggacaggaa	ggcaaaagac	ttgaatctt	aacaaggat	taagaacagg	atgtcatctg	540
tgagcctgtc	acagtgggtt	tgcagagcag	gagaacacag	acaggattag	ctataaagtt	600
gttacattag	ttattntatt	ggagcataca	atacttaat	agtcttaggg	caagagaat	660
gaacagaaaat	gaccttataa	gagccagagc	tgtagccaca	gctttcttg	tgcttagttt	720
gctagttcac	tcttccagg	gcagtcgtt	ggattacacc	aaattgtctt	gaaaatgcta	780
gctctactgt	ccctgtctat	tgtcagcttt	gcaatgtgca	tagtgacagg	agttgcctgg	840
gaagcttggg	gcttatgttt	tgcagatcca	ttgttaattaa	aaaagaattt	taaggagatg	900
gaggcacggg	gtgagggta	gggtgagtg				929

<210> 42

<211> 943

<212> DNA

<213> Rattus norvegicus

<400> 42

ttgaaaaccc	caacctggaa	aangngtntt	nccggaaat	tcaacctgcg	ggcnaatgg	60
gtaaaagggc	ctaccttggc	ttngaaggga	atntcctgaa	ggnnaatcc	caannttgg	120
natcccaatt	aaggntnaac	nggttaatt	tgnntccnc	ntaccnacn	ggttncctg	180
tatactaaag	ggctacaat	taatgctca	naagggaccc	ccaaatcctng	gcnagaactt	240
gggttaaggn	ttccattagg	atttgcattc	ctntaccctg	atcttgcaca	tntnttgaa	300
tgnnttgcca	aggaacngaa	gttttncct	naagntagca	cacagcagng	accaaggatt	360
gaaacccagc	nagtgcttgg	aggtaaaaga	tcacttccnt	ntcccttagt	caggancntt	420
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cgtccactaa	agctgcctcc	aattcaaaact	ggattgagtg	acaagtggct	tgggtgtctc	540
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ggcagactg	gctcatcctc	tgttttctc	tgagtgttgg	ctgtgcctt	ccacacagac	840
tctctgaagt	caaggagccg	caccagca	tcagttgtgg	gccataatca	agncangact	900
gaaagttgcc	acctgttagng	gcccgaagca	aactgagatn	ttt		943

<210> 43

<211> 867

<212> DNA

<213> Rattus norvegicus

<400> 43

agggaaaccnt	ttaaaaaaaaa	aggggggggg	gggggggggn	ntagnggcaa	aaaagatgan	60
accctcaagn	cgggggggggt	taaanaagga	atcgatttc	ggcttgnac	aaataaaagga	120
gttttngng	natttccccc	ntgtcgttt	tntgnacat	ccacggttga	ccgacgacgn	180

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acggaccgac aaccaanacg taaaggggaa ttgtggaggg gttggaaagt tagatgcccc
gacccaggac gtgcggccan cttccggaga cccaccttc ttgtngccg gnnccggcgcg
cagcgnagcc attccacccg gatccctata gcnngccagc cttagcaggcn gaacaccagc
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gcacttagta ctttttggca ctgtgctgta taaatataaaa tggccacac ttaacatctt
agatgttata tctaaagata tgcacatcttta aacttcgaaa ggcacataccc taaaatttca
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<210> 44

<211> 303

<212> DNA

<213> *Rattus norvegicus*

<400> 44

ggaaatgatt agtccaagaa atatggcaga agaagggagt tagggtttc aaatttagaa 60
agtggaatcc acagagttcc ctgtacagag aatataaaaa ggactctggg gtgtcagaat 120
ggtgggcatt aacctgatct tccacttgag ggttaaggaa atgattagtc caagaaatat 180
ttqagcagaa gggagttagg gtttcaaata taggaaagtg gaatccacag agttcccttg 240
acagagaata taaaaaggac tctggggtgt cagaatggtg ggcattaacc tgatcttcca 300
ctt 303

<210> 45

<211> 840

<212> DNA

<213> *Rattus norvegicus*

<400> 45

aaaccggng	aanaaaaaan	gaaanngang	gcnnnaaaa	agttnngaca	aaaaaaactt	60
tngaaaaaa	gganggggn	aaggcaggn	nccnactnaa	aanggnctt	tcnaagngng	120
anagagntgg	naatnagnaa	naggacattc	tttnaacctc	changgngn	ngaannaat	180
ngggattttag	cngccaccat	tagggangaa	gttngaattn	nggggcccgn	gnagttaaa	240
angattcccn	ggttttttaa	aacagagaat	acctncaggn	acagatnaac	ccgagattgg	300
ttccctngaa	aattnnngan	aaagataaan	gtaggagcat	tcaaagtagn	anggtaaaan	360
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cgcacntaga	tccaggcgnt	gggggggggg	cgggggcgcgc	ntngcagng	aagntnnngc	540
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ccgttccgga	ttntgcgttc	acaaagggag	gcgggactca	cgacntgngt	atcntngng	660
tcccaacccc	ggcccccnac	cccnacccccc	nttgcgttc	tggcattcgc	gttctttccg	720
ccgtctccct	cgccggccgn	ttntctgcgc	ctggtgatcc	tttcgcatg	gtcctntgga	780
gaaagaaaaa	atcttaatt	tnctagggac	gtcctttcc	tgtagtcgta	attgtagaaa	840

<210> 46

<211> 893

<212> DNA

<213> *Rattus norvegicus*

<400> 46

gagaaggann	aggngggng	agngaagana	gaggagggaa	gaaangaagg	tggaganaag	60
tggannaaaa	agagggagan	ggagggagaa	ntaaaganag	ganaagagng	gggaggaggg	120
gnagnatagg	agagggaaaga	aagganggan	agaagagaaa	agaanganga	gagaaaggaa	180
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aagganttag	naggaaagga	ganagagagg	tagagagaaa	anaaagaggg	aaanggaggg	600
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ggagggaaaaa	aagnagagaa	gaagagnaat	gggaaggang	nagtagnaaa	agaaaagnag	720
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nacccccc	cccccacac	acacacagcc	tttgcgcgg	cggaaagtgc	ggttggtcca	840
ggagcctgtg	gtcaatccag	tcagtagtgg	gcgaggtgt	acatctgtgt	ccg	893

<210> 47
 <211> 789
 <212> DNA
 <213> *Rattus norvegicus*

<400> 47

taaaaanang	gnngannanc	tnnaaaaaan	tntcttngga	attnncagga	nggaggntaa	60
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cgtttccana	gncaaccatt	ctgggnnc	caaggttnga	ngagntccgn	tcaaggngaa	180
accttttcaa	gaccaattaa	ctaggggatn	agaggcgggn	tggtttntga	ggggcgggct	240
gctgagaaga	ttcggttggg	gaccaggag	tgaagggttt	tnacctgtgt	ntntcggaa	300
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agcgtttact	ttttnttgc	cgcagccat	ttgttntgt	tggtttcttc	ngaatccgg	420
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ttccggcagn	tacganttt	caacaagagc	cagagaaggc	gggtgcagag	nttcattagg	540
acgntcgaa	acccggcgtg	acttacttt	tccaaagccca	ttggttgtat	agaatgtat	600
ctgacaggga	ggcgtgttca	cgctgtcg	ggcgggagcg	acgggtggag	ttaacgacga	660
aagctgcgcg	cgcagccatg	acccctcaca	gccacntatc	ggagggaggg	gcgggacagc	720
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ctggttacc						789

<210> 48
 <211> 872
 <212> DNA
 <213> *Rattus norvegicus*

<400> 48

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cggggaagga	aaanggggct	ctnaaaaatn	gttantgg	tggngcctt	agggggggcc	120
catgngccag	gaangcagat	tcaaaaatgt	tccaaagtgg	aaaccanggt	tggnanaggc	180
cctccngnc	gtnaaggagg	agaggagaga	tggagttca	ggtgtt	ccacccagtg	240
ttcccaggga	acacaaaacg	gataggtcac	cntcaatna	caaggaatta	aaagcttgg	300
tgtatngg	ggcgtcttc	caaagccacc	agaaaatcc	gagagccgn	ggatcntacn	360
caccagagg	ttcataggg	gggcantatt	aggggtgtc	ccttgtgaga	ggaagtgtgg	420
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gtntctctcg	gtctcttct	cngtctctnt	tcagtcttnt	cagtctct	cagactct	540
ctctctct	ctctctct	ctctctct	ctctctct	ctctccngc	tgcnttcaga	600
tatagacgt	gaantctct	ntatccagca	ccatgtctgc	ntgcatgtgc	ccatnttcc	660
caccangacg	ataatagct	aaacttnt	actctaagcc	agcctcaatt	aaatttntan	720
gagtcaaacc	agcctcaatt	aaatgtttt	atttctat	gtcacagtgg	tcatggcatt	780
tcttacagc	aatagaaacc	ctaactaaga	cttgcgaaa	cctcaaccac	aacttcagcc	840
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<210> 49
 <211> 785
 <212> DNA
 <213> *Rattus norvegicus*

<400> 49

tcgtaanttt	tnatccacccn	gtanangatn	ttccatgcca	ccatgtacgg	ttacgaggn	60
tatagcgtgn	acngtttgg	agtngctaa	aaggaaatgg	agacntatt	tnttggttt	120
gtgaccata	acttcggaaa	ggttgtt	tatccggca	caaccacngt	gtagcgggt	180
tttttgcgg	cagcagcaga	taacgcgc	aaaaggatn	tcaggagatc	ctttgat	240
ttnttcgggt	tctgacgntc	atgttgtgt	gaatttgtg	cggataacaa	tttcacacag	300
aattcaaagg	agaggagcc	atataaggg	ggaaaaaaa	agaaggggaa	agcattagtt	360
taaaaagtt	agagaacaa	gtatgttt	cttggatgg	caaccaaaga	agcntgcag	420
gaatggcgg	taaaagggt	aagagtcat	aaacgtctt	tgtccaaacc	ttaccggaaa	480
catgcaagga	atttctt	ctggccagga	ttggattt	ggaaaggct	tctcaagcnt	540
cccccggct	tttatggca	gaaaatagt	cgactata	agagcgtgt	tctcaagct	600

tgtccccaaat	agcagaaaaag	cattgtccta	aattccttaa	aaggcaccgt	gaaataaata	660
ttacgaggac	acgatggcac	aagaaggagc	tttcaactct	gccaccagaa	cagttatact	720
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ggagc						785

<210> 50
<211> 889
<212> DNA
<213> *Rattus norvegicus*

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<400> 50
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gcgca gggatagngn gttcnggntt cccacangaa tttgattttt ggaatcacaa 180
cagtn gccgnaatca cgagtttgc gcttntttc ctaccttana ttcataatan 240
agtan tttttttta ttgagnaang ttttnacagg ttttagtaaac atgaggacag 300
ttaag ttgangatta ggaaggagag ttccggggga cagaatgtgt gtatntca 360
gcact acccggaaaga gttgcagtca gtttgaggaa gggagcggat ttctggagg 420
accaa cagagagaaa aagcatttac tactgattaa gcacacaatc tctggattca 480
gggtg ttaccttta tataaaatgt ctccctaactg cgtgactgtg tgacttttgtt 540
caact ggcacttgac tgggtgtgt gcaacatggt aagaggacca actttnttc 600
tttat ttattatita tgtcacgtgn acacttggtg cttttgtttt tgttcttaatt 660
cgcat atatgtctgc ataccacgtg cattttcgat gcntacagat gccagaaaaag 720
cgagt ttccccctggg antggagttt tagatggttt taagtctctg agtaggtact 780
gtgaa cttcagttt ctctggaaagg gcagaaagcg cttttcaat gctgggccat 840
ccagc ccctacttaa tttataattt tattttqaqq gatgtqctc 889

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<210> 51
<211> 947
<212> DNA
<213> *Rattus norvegicus*

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<400> 51
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jaaga nggaaggnta acataggagn caagaatana aaganaaaaa gaggttagaga 180
gagaa cgagaaaaga taaaanaaag antanaaang aagaaaagang nccagnanaa 240
caga aanaagatgn cgtaaaanaa gagagaagat aggnaaaata gaggagaagg 300
cagga ngggagagc agcgaattnn agataaaacc ggagganagn nagagaaggn 360
tngnn aaggcaaaga cagnanngag nacggtacnt gccccagaag gnngaagaan 420
jangg tgagggnnng cacngncnt tccccttagg aggncccg cccagagatc 480
ccnag gncaccgagt tggatacnag attatncacc naggcagggaa angantatng 540
ngatt cggggngggg tcacgggtg agaaataan tcannaaaana gggacgngg 600
ggngg gaaactctng acagaatng caagcangaa gccagccnca cccaagcccc 660
aagca gcnagagnt tgcangcgg naagttccaa tcancgnagt catggagnng 720
ggngg gccccnganc cantgaggg aggcaggaaa ccatatcnag cccgaccnng 780
ntgc cctganacac ccggagaggt aatttttatt tnacggaaag cgtccagnca 840
tgggg ccgaaagaga cggtaactta gtatacancg ctnntgctnc gagttgttnng 900
tnat gnnagatctc acaaangaag ctnanaaqta qatatqt 947

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<210> 52
<211> 860
<212> DNA
<213> *Rattus norvegicus*

<400> 52
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attta aaggggnggg angttttcc ggttctattn ngccnattcg gggttacact 120
ccanc ntgtntttt ttanccggcc ggtttaaaaaa tgggggggga ttatgtcg 180
tttnc cnacagcaca gccctgtttn tcttcgttcc ngaaaaaaaaa aaattttct 240
caca a ttntttaaa caggatttnc ttcaaccatg gattaataca ttccgggtgc 300
ccccg gtttggggggata gggatgccag caggatttag ggtatgcccatt 360
tttagt ntctggccct ttaggagagc ttggggctaa ttatgtgacc gattttaaga 420
gttg ttgtgatcc agggactcac ggatcagccct ttatttata aggacactgt 480

ggaggagaga cagaggctga gtcgcattct gatgtcattt gtgctgtgt ggaagttaaa	540
aaaaagctgc agaagtcagc aaaacagatg aataccaaga agggcagtgt gagtacagga	600
atggagagaa aagtcaagt ccagcttgg ttaactccct aggatcagac anttctgcgt	660
aaggacgggt ctacagttt aca gaccaca gagcaangtc aaacagcaaa gtggttcat	720
ggcaggcagg aatggAACa tttaactgg aacactgaac ccacccatgg ccaaacttagc	780
aatgaagctg ggtgtgtgtt cacatgcctt taattccaaac actcagggga cagatntaat	840
gagtttgagg ctagactgtt	860

<210> 53

<211> 191

<212> DNA

<213> *Rattus norvegicus*

<400> 53

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aattcctcag gatggggaaac agccattggg ctttttagtag aggaggggaca ggcccttttg 120
cagcaacagt tctccctctga atgttggatc tccacacctata cacatggggt acttagcctt 180
atggatgccc c 191
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<210> 54

<211> 988

<212> DNA

<213> *Rattus norvegicus*

<400> 54

ttttgggnna	cgggtnccg	nantatgaan	ccnttcccg	gttttttaaa	aancccngga	60
tattcgaaaa	tttgggttt	nnacggcctt	tttttnagag	gccaaatncc	cntntnaang	120
cctttatcc	ttccnntnt	gccccncttc	naatttaggaa	gcntggtttg	nccgantntt	180
aaggtttta	gtcntccttc	gttnnntttt	cccttntttt	ttccctnaag	ttataaagcn	240
ggtagatnngt	ttgccaggn	tctnttgac	ccgtcatngc	gggttncggn	ttacccaggn	300
tttggttccctn	ggccggtncc	ttccaatttt	ggantntccn	ggtcngggngt	ccnattncct	360
tgnaacngntt	ccacacntna	tgacaattaa	ttgtttcctg	tgttaatttg	ccccggactt	420
ntggattctt	ngnancaggg	cctntgttcc	atggaagcaa	actcccttaa	ntattttacca	480
ggttgtatga	ttaagaaaagt	antcatgntt	ggggaaaccca	cntgtttttt	tcccaggatg	540
gaancccagg	attttggaaac	tgcagaggt	tcagggcttg	ggaagcggag	gcaggcaag	600
aatggagtg	actgtccctt	tgcaatatgg	ggtttgccctg	cctgtcgct	cctctcntgc	660
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tgcccttccg	agcagaaaagg	gacagacgtg	gggcgatgaa	gttgcstatcg	tttttttttt	780
tttctgcaca	gactgcaaaag	tgtgcagagg	gaggggaggct	gtgcaaaaaaa	aaaaaaaaaa	840
aaaaaaaaaa	aaaaaaaccga	ggacgcagaa	gttagactgc	tgacccattt	ggtgcacgtg	900
tgcccatgga	gggaggggac	cttctcaaaa	gggttacgc	agcangcatt	gaaagtnccc	960
cacntgttagg	gnccgaaagca	actgagat				988

<210> 55

<211> 665

<212> DNA

<213> *Rattus norvegicus*

<400> 55

<210> 56

<211> 857

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<212> DNA

<213> Rattus norvegicus

<400> 56

aaaaaaaagaa	aggaaagggg	agananaaaa	annangngan	aaaanagana	ganagaggna	60
agaggaagng	agggngaaaa	gagaggagan	aaanaagagg	aaggagaann	gaggaaaang	120
aaaggaacaa	aaganaaing	anggaagana	aagggagaaa	aaanaagagg	gagaaangga	180
ggagggaaan	agagaanaga	ggggagaga	anncagagaa	nagaanngag	aaaagggngga	240
gacnaanana	gagggaaagaa	aagnaggag	aagagagggg	agaanaaaant	tgaagaagaa	300
gaagangaga	agangagnag	aggaaganga	ggggagaag	aagagggngga	ggagaagaag	360
aggagaggag	gaggaaggag	aaggaggag	aagagaagga	ggagaagag	gagaggagaa	420
ggaggaggat	actanggagg	ttgttcaat	aaaagagnng	gatntaagat	taahanaagn	480
aataatgccg	gttntatct	gttcgggggg	ggtccttgtt	ctccaaacac	aganntggc	540
cagttntca	aaattnaant	gngaagattt	cttggntnga	gagcagntca	gattnantng	600
nattntttc	tagtttcaa	cacaanctt	gtntaacaa	aganganga	ttchaggana	660
actcgnttt	nttggggagg	agactttgtt	ccttcnatg	aagatgcagg	acnggaaaga	720
cgcagggtgt	gaacaggaca	cagnacgct	tnngtntntg	tcngcntcag	cngcgtggga	780
atgagtcaga	gcagcacggg	gaggtgcctg	gatntaagct	ttctggtagg	gagaacagag	840
tgccaggcngc	ggcccaag					857

<210> 57

<211> 902

<212> DNA

<213> Rattus norvegicus

<400> 57

aaaggggng	ggaagaanga	aaagggnaaa	cntngttt	gaagccnnca	nnaaagnnaan	60
gncgaattta	anaagggggt	agggaaaaaa	aaaacanaat	attccntcct	tagccatnaa	120
ccgaacttcc	ngcaaggaaa	aaaaatttgg	ngggngtaaa	gggcacncn	tcccacaaaa	180
ttttgntaan	tttgggcgca	aattcangca	gnnttngtt	ggaaaggngn	ananacaaaa	240
gggatttngg	gattnnaaa	atcngngttt	nnggcaggnn	atccnagaat	tngaatcgaa	300
cgncnacccct	ttattnagc	agttatttan	ggaacatgg	gaggnacca	tttcaaacc	360
nggatcgggc	cnngagtnng	agtgttcage	ccacngcctt	cnaacantac	cgggataagt	420
ttttccctgn	gccagagacc	catccangtt	ccagcaaaag	gntggtcate	tnnggcnagc	480
tccnnagagtc	atcnggggtt	tctccagcc	nggggccaat	gtcgaaggc	aggttnttt	540
tgtctccagc	ttgttcccn	ccgnngggagc	ctgtcaagc	tgcacagnac	cagantagtg	600
gtcatntcng	ctagctccn	ttagctccnt	gtccagggg	cttcctggca	ctggattagt	660
ggnggactca	gcttgcctt	ttttcagga	gaggttagat	tactaatcat	tcagatgttc	720
ataagtcaga	acactgagca	aagcaatagn	ttctcctcca	cntactgant	cacacgtgca	780
caacagccac	acccgcaatg	cttnntaggg	caggtccagn	gnactttgt	tttaactatt	840
tntggctctt	tattaatcag	cacataaata	cgcttcgtt	ctccttttc	aatatgnatg	900
tg						902

<210> 58

<211> 852

<212> DNA

<213> Rattus norvegicus

<400> 58

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aaatgttccc	agacaaaaag	ggggggggna	gttnaattca	ngatccctna	ngaggnggaa	120
atttttnnnn	tattnaggat	caggataaat	angaaaangg	gnanatttt	nnnangnggg	180
tttttttttt	tttttttttt	tttttnngng	gnnnnannan	annnnnaaat	ggcgnccggc	240
atggntaatg	ggaanttgg	gganaattac	agagatttt	ttttcccatg	gnnttccagg	300
atgaattcag	ntaccaacca	ggttggtacc	agcattttaa	cattcgagtt	agacatcaat	360
ggttaggtcg	ggagtggag	gttcggggcc	ngacatataat	tcntggtgaa	cccgagtgcac	420
cttnngttt	ntacaaggag	cttgaggtag	tcgcccacca	gtagctgtca	ggcaggtggc	480
ttaagttcag	aaccgnttcg	tggaaacccga	gaagcagaaa	aagacataag	ttntgcngct	540
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nacangagggc	cgggagcaac	aantccacag	ccagcccaag	ganataaaaa	ggacttgggt	660
cagttctgna	ccagttggag	tcaagatgg	gcccctcaaa	gtcccagcag	tgaagggcat	720
ggtctccagc	nnacagtgg	accttaaga	ggtggggact	tgttaggagga	tttagataat	780
tggggtgtgc	cttgccttcc	nacntcgttc	tttcccttctt	tatggcctt	atgtggacaa	840
gattgtttct	gc					852

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<210> 59
 <211> 884
 <212> DNA
 <213> *Rattus norvegicus*

<400> 59

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ntttgtngtt	gtttcctcng	aggcggagng	tcaaaaanaga	acacnnctgg	naaaccffff	120
ttaaaaanaca	aaaatttgc	ggggnnngng	ngttacaaaa	agacaggatg	ttttccgagt	180
cggattcaat	cccaccacaa	catggggttc	acaccatgt	aaggaatcgn	tgcccttttg	240
ggggatcct	aggggttana	nttccaaata	nngataanaa	ttttttaaa	aatttaattg	300
tanatattta	ttanataatt	taataaataa	tatttgiana	nannatgtt	ctngcgcctt	360
gnggactgg	agttttttnt	ccnnattnna	actttccag	nactnggtag	cctatgtnt	420
tatcaacccc	nttagaagct	gccttcanta	ttnaactcat	actgttctc	gataatcngg	480
ggagtagctc	cagttngcta	tgaagctcg	gaaaggtagg	cggacatccc	aggcttagac	540
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tntgggtccc	gtagttccgg	tcgcccaggag	tagtgtattt	cttaggacca	ttctgggtgg	660
aatgcacat	gtgggtctta	aannatgtca	ggcagggcct	ggcaccaggg	tctggcggga	720
agcctcacat	accgttnaa	tgacttcata	tgcttagaaat	ttgtggggaa	acgatgcaga	780
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<210> 60
 <211> 955
 <212> DNA
 <213> *Rattus norvegicus*

<400> 60

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ggnnngttct	tctcttggan	cgcntttgt	tcgaccgggg	tgactaaggn	catgtngggg	180
acgantaatt	gtttccgggg	gcnngntcgc	accttccnan	gnngngnggg	tttgggtctg	240
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<210> 61
 <211> 1107
 <212> DNA
 <213> *Rattus norvegicus*

<400> 61

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atccanaatt	naattccgga	aatttacaat	aatttgaatt	ntagtttcc	caattnaat	180
ntcagtagtt	tgnnntttgt	tgccccnatt	ntaanatcag	acccgtccaa	tcacccaatt	240
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aataaatcgc	ccccccccc	ccgcttgcgt	aaggcgcgt	gtatctctgg	cattgtgtgg	960
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<213> Rattus norvegicus

<400> 66

catnggagtt	cccaatggnt	tccnntnaann	ggttnnttc	aggttggca	ncntttagga	60
attgaaaatn	ttnnnttgga	ttcccttaga	atttgcattcc	attnggaaa	ttttttattt	120
ccngaacagt	ccantnttaa	aattgggcct	nttgggatta	acggattcca	aggttgcaac	180
anattggcaa	gtttnnggac	aggaggttc	aantggntaa	agtggataaa	tngtgaattt	240
tggagangga	attgacttgg	ttgggggcca	aaantagta	gcattttgcc	cggaggggtt	300
attgcattet	gttttgcgt	aanatgaagn	tacttgacag	ctttgagata	agaaggagac	360
ntaattgtct	aaacattttt	agtgttctat	tctgcccggag	ttttggagag	ggtatatgcc	420
ggtcagggag	ggagccagaa	gcccgttaaca	ttgcaagttt	ttcaacatgg	aaagctttag	480
gttatctctt	tgccatctta	tgctcggnnta	atgatgttaan	ccaaattgtta	ttctgggcac	540
agctttccca	tgtgtcttgc	gaacagtctg	ggtttgtggt	tntaaaacaa	catttgatn	600
tagtggagg	cttatctaag	gagcttctta	gcatttggtt	tgtaattttt	tttagtattt	660
tttcagctac	ccattgctac	atagtaaatg	tacaaaaaatt	tagtggatta	aaataatgtat	720
gtttggtttgc	ctcacgaatc	tttcatgttg	gctgaagtttgc	ccatttctgc	ttctctctgc	780
tgaacttggc	atcaactgag	agggttggaa	tcatctgaag	atgggttag	ccacacctcg	840
cagttgatat	tggctgtcag	ttggAACCTC	agctgggttc	agcatgcata	agtaagcatg	900
tgtcaactttt	ccaggtttct	gtcttacagc	atgggtgtt	ggttctgaag	ggccatcaact	960
ctaattggtgg	ctgggttccc	agcgagaacc	agttggancc	aaggatagct	tttgggtgact	1020
gaaagacttt	aacctgttagg	ttggggccna	gctanaaaaga	gat		1063

<210> 67

<211> 815

<212> DNA

<213> Rattus norvegicus

<400> 67

cccccccccc	aaaccttcct	tccaaaccct	tnnggggtgg	aaaaacattt	ggcaangggg	60
caaatttana	cccttggaa	tngtngccn	ggnnaaggtn	cngtcccc	aaagccaaag	120
gggggggtt	tccaaanatt	ccnggggttt	tttnnggggg	taaagggnnt	naaaggtnaa	180
aaaatgttcc	cggngcccc	anacttccaa	aggttttccc	tttnaaaatt	ccnggccttc	240
cgggggnccn	tntgtncccc	ccnttcccn	aaatnncntt	nngaaaaggg	ttnaanantg	300
tttnaaaancc	cnaangttaa	angggnnnat	nnaaangttt	tccctnnccn	ggggngggna	360
aaaaggtttc	gcgcgganac	cnntgatgcc	caggttcagt	ttccccggag	cttggggcca	420
gaccgcggc	gcgcctnggg	tgtggcggga	gcgcgcgggc	ttgcgcgggc	acggcttctc	480
cccgcccccc	actccctcc	gccccggcgg	gagtaggttc	ttccggctcc	ggtctgaggc	540
ggtgccttgc	accttctgac	caggatccgc	gggtccccgt	gctgtggtcc	cgggaggcac	600
gcggggcctg	cctgctatac	cggttttgc	gggcgcggct	ccctggagcg	gtagggtcgg	660
tttgggtgtt	gcacgctcgg	tttgacgttt	taatccggag	gagttgtggg	tttcctcgaa	720
tctcaaactg	ccttcttccc	ttttgagact	tgaaaatacc	cgaagcctgc	tttgtactga	780
aagacnttac	ctgttaggtt	ggcagcttaa	aagat			815

<210> 68

<211> 1034

<212> DNA

<213> Rattus norvegicus

<400> 68

aaaaaaanagg	tttccccngg	angtccctng	gggntcnntt	tnngancntn	cgttangggg	60
ncctncncc	tttccccctt	ggggaggggg	ntttttaaag	cnannnnntng	ttttcnntn	120
gggttaagtn	tttccccaaa	agttggttt	tnnaaaaanc	ccctttnncc	cggacgtttn	180
ccttncnccg	anaatatntt	ttgggccaaa	ccngtttagnc	gggatttccc	aattgcgnnc	240
cccttgnaaa	cgggttnccg	ggggngntt	tnaggggtt	aacngggttt	taaangtgcc	300
aaaacgggta	aattggaggc	atttngnaa	tggcttttgc	tnaaccnntc	ccttggaaa	360
gggtgttagt	ttttaacgggg	naaacaacc	ccgtngtagc	gggtgtttt	tnttnccaa	420
gcgcggnta	agccncggaa	aaaaaggatn	ccnnggagacc	ttgnatttt	nnnggggttt	480
nacgnatnt	tttttggaaat	tttgggggaa	taanaattt	nnaccnngaaat	ttttngnggc	540
cncncnnnng	gnnaaaaatc	tnannannat	tnggttattt	aacatttctt	ccntgcatat	600
ttatngangt	atgaccctt	aaacaattaa	gtacttgct	tcagtgagg	agaaagtgc	660
tagctcaaa	aagacttgaa	gtgcccagg	tgtgtgtgt	tgtgtgtgt	tgtgtgtgt	720
tatgtgtgt	tgtgtgtgtt	tgtgtgtgt	taacccagag	gggtgcccac	ttgctcaaaa	780
gagaaggggc	agaggaatat	gagggaaagga	ttgtgggagg	gagtgaccag	tagggaaaca	840
gtgagtgtga	tgtaaagtga	ataagtaaaa	aaattaaatt	aaattaaaag	taaataaaat	900

-23-

gtctacaaag tcaattactc cttcccttc ctccaccctt tcttctaata ttaggcaaaa	960
acaaacncaa aaacanaaaac aancaaactg aaagactnta acctgttaggt tggncagctt	1020
gaaagagatn ttcc	1034

<210> 69
 <211> 186
 <212> DNA
 <213> *Rattus norvegicus*

<400> 69	
agaccacctg ggtggaaact cctattctta caccaagctg cctctgtatc cacagatacc	60
aagaagtgc caccgttgtt ttacttaact catggccac ggggtgagct gaggtctcct	120
tcctgagcaa gatggaaatt ttacttggtc tgttaactag cgtgcattga atggangaca	180
tatgtat	186

<210> 70
 <211> 1028
 <212> DNA
 <213> *Rattus norvegicus*

<400> 70	
aaagggacn ttttaagcnt ttnnaattnn gttncnaan aaggatttgc atttaccacc	60
cttaaattta ggnattttt aatnatttca acccnnntgca ggcagtttgc nccatgttnt	120
gggaaagttt taacaggatg gttattna caaaacaggt tttttcagac catttgcgna	180
ntatcttgcgaa atttcccgat tttttaatttntt tattntaang atattntagt tnnnaatttnta	240
tgacttcaat ttgtatnac aggttcttaa caaaacaggtgt gtaactgatg accttgcggcc	300
agcatttaaag gttacacaca tcatacgaaac actgaagaaa atgtctgntc ttttattttc	360
cccttttctc tggtaattt ctttcaggac tcctttgtcc tgagttgtca ggccttgc	420
aagatggtn atcttatttc tgtttgcaca tggttgcata tcntgcctga cagttcttgc	480
ttaatgcaga aaccacgaa aggttcagtt tgtaactggc tcccttnta gttatctgac	540
aggatcagt tttcaagctg tagccgtgt cctcagagag acctctgcggcc atatacagca	600
gcagtcttcc tcatcccacg cctggaggtt ctggaaaga tttgactttc tgagttgttc	660
agggtcagag accatgtatc aagccctggc tctattttt gagaatggatg ggcacatctggc	720
acatctactt agatgcagaa atagtcagaa tgaagtgaag atgtaggagg agtcgtgtgg	780
agaaataggc tctctgaaag gaggcttctt cttcaacttta taagctgttag tgcattccct	840
tcccaagtgg ctctgaaact gtgttagaag acatggccctc cccagagctt gggaaacact	900
taaataaggc tgctgctcag atgtcagcac atttacgct ttacttggaaacttctgctt	960
cctttcccta tttctccaaa tncanntgaa agacttgcac ctgttaggtt gggccagctg	1020
aaaagatc	1028

<210> 71
 <211> 1034
 <212> DNA
 <213> *Rattus norvegicus*

<400> 71	
aaaaaaanagg tttcccccngg angtccctng gggntcnntt tnngancnntn cgttanggg	60
ncncnncct tttcccccngg ggggaggggg ntttttaaag cnannnnntng gtttccnnntn	120
gggttaagtn tttncccaaa agttgggttt tnnnaaaancc cctttnncc cggacgtttn	180
ccttncncngg anaatatntt ttggccaaa ccngttagnc gggatttccc aattgcgncc	240
cccttgcnaaa cgggttncngg gggggngtnt tnaggggtt aacnggggtt taaangtgc	300
aaaacgggta aattggaggc atttngnaa tggctttgt tnaaccnntc ccttggggaaa	360
gggttgttagt tttnaacggg naaacaacc ccgtngtagc ggggttttt tntttnccaa	420
gcgcggnta agccncggaa aaaaaggatn ccnggagacc ttgnattttt nnnggggtt	480
nacgnatnt ttttggaaat tttggggga taanaatttt nnaccnngaaat ttttngnggc	540
cncnncnngg gnnaaaaatc tnannannat tnngntattt aacatttctt ccntgcataat	600
ttatngangt atgacccttt aaacaattaa gtacttggct tcagtggag agaaagtgtct	660
tagcctcaaa aagacttgcgaa gtgcggcagggt tgggtgtgt tgggtgtgtg tgggtgtgt	720
tatgtgtgtg tgggtgtgt tgggtgtgtg taacccagag ggggtccac ttgctcaaaa	780
gagaaggggc agagggatata gaggaaagg ttgtggggagg gatgtaccagg tagggaaaca	840
gtgagtgtga tgtaaaagtga ataagtaaaa aaattaaattt aaataaaag taaaataaagt	900
gtctacaaag tcaattactc cttcccttc ctccaccctt tcttctaata ttaggcaaaa	960
acaaacncaa aaacanaaaac aancaaactg aaagactnta acctgttaggt tggncagctt	1020
gaaagagatn ttcc	1034

<210> 72
 <211> 824
 <212> DNA
 <213> *Rattus norvegicus*

<400> 72
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 aangggaaa angtttgaa atcantgtaa tgaggttcca aaaattgagc aggaaattgg 120
 atgntgttag gagaacccn ttcagtnttgc tgcaatttgg tcgcacagc ttaggaccgn 180
 ttcccatca cttgtgccag cgacatcca gntattgagc cntgnatcat ttatgggnaca 240
 aatttaggaac acacaacaga gatccgctt ntactgcca tggtcgccaa actcaattgg 300
 gggaaagtaat cctccagacc gttcgtttg cacgtnttagg aagccacagt gaaaacacaa 360
 aattcgtgga ggcgactcta accaggaagc ctaatccctt agattcccg gacactgggg 420
 caggcgtcct aaaaacagct ttgtgggct tcagtctcc tgccgggtcc agtccgggtc 480
 ttgggatcg ccctcgccgg gaatgtccgg gactccggtc ggtatcttt tgccctggga 540
 atttccagcg tggaaaaaa gtccacaaac ttacttcctca ctgcctccctt ccctccctcc 600
 ggccttctc ggtgcccacg caccggccga tcgaacccga ggatgagcat agggtgtatt 660
 tttagcgtgc tgggttccc cgcccccctc tgccactta gctggcaaga agaaagccag 720
 cactataaag gaggccaggg ccaaggactg gcctctt gctcactgagg tcagacgcga 780
 gctctgaaag acttcacccgt tagtttggc aagctgaaga gatc 824

<210> 73
 <211> 774
 <212> DNA
 <213> *Rattus norvegicus*

<400> 73
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 gagnnnnnn tgagcacgng gcantccaaac cgnntcaaggt cccgnnttcgg acggtcacac 120
 antaggttnt catntggatt gcnngngttc cngttggcat cgggaaaaan tgagactgtg 180
 tcggtaccag agntaggatg gcnntccctt cngccccgg cctntttggc gccttgcgt 240
 cctttccgaa cgggcccctg gctctccgc ctngggact tgacatntg gggccccagg 300
 atggcgcttc cgggatggcg ccagcgcgcg tacgtcatca cggagcgtcc atgtgttctt 360
 tctgtccaag cgcnttaggag cctgcgcgtt cttccagcaaa ggaagatgtt ggaccaaaat 420
 gtagaagcac ttaacatgaa cgtccaaacg atgaccaatc acagggcgat atatgcgt 480
 ggcgaatgtt ccaatcatgg ctcataagca atccggaaatggccaaatataactatt 540
 tactaatcca gggttacaca gtgaaaccct gtctcgaaaa ataaacacag ggctggagag 600
 atggctact gattaagaac actgactgtc cttccagaag tcttgagttc aattccgagc 660
 aagcacatgg tggctcacaa ccattctgtaa cagattctgg tttatgtnga gacaactaca 720
 gtgtactcgat attgaaagnt ncccacctgt aggttnggca agctaaanga gatc 774

<210> 74
 <211> 248
 <212> DNA
 <213> *Rattus norvegicus*

<400> 74
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 aaccgacttc tttttgttgt tggtctgtat ttttggggg gagataaagg tctcaactgtg 120
 tagctcaggc tgggtttgaa atcaggatcc tgaccctcag gaatgttaaa gtgcctaaaa 180
 gtggngacaa attatttac gtgccttgc aagacttcac ctgttaggtt ggcnagctag 240
 aagagatc 248

<210> 75
 <211> 833
 <212> DNA
 <213> *Rattus norvegicus*

<400> 75
 aanggggta tnnntggagan atnctaagnt cccaaagca nttaggattt ctnccnnnng 60
 aattnttaag ctttgcatt aagtantaat gccaaaatga ccccaanata tngntcctt 120
 antgnntaa aaangaggat cttcatttgc catanacgccc ntatgtaaa gcaactgaac 180
 aagattttaa attggacagg tcacaancgg gcgtgtgcct ttaatcccag cactcgntgg 240
 ctgtatagaag cagatgcatt tatgtgggtt tgaggacagn tngnttnacg tagagatcc 300

-25-

ntatatactgt	agggctttgt	agagaccnta	tctcaaaaaa	caaaagcaaa	acaacagaga	360
aaaaatcaat	tgaccatgtc	ccaattacct	ttatttatct	gtaacctatc	cttagttata	420
ctcgtaatct	ttttctctct	tcagttgcg	tacgggacag	cagacctact	cacaacccaa	480
gctntaaatg	atgagcgtac	tcagccaggg	agttcaccc	cacttaaccc	cataagatgg	540
cggcagcgc	tcttcaccca	ctcaggcgt	aagcacgc	cacgtgatgc	gctccagtc	600
tcgcgcgcgt	ggctgacggg	aggtggagat	agaacgaggg	tgtcggccat	tttgcgtctg	660
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ttttttttt	ttgttttcg	ttttcccccc	agttctttt	cgcctctntt	ctgcatagtc	780
tgttagtgcgc	agttgaaga	ttccacctgt	aggttgggca	agctaaaaga	gat	833

<210> 76

<211> 880

<212> DNA

<213> Rattus norvegicus

<400> 76

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ccggattaac	tccaaaggcca	aaattccgag	ggggaaatcaa	caacaaggac	ccaaaccggat	120
taaggcgggt	tcaaacaac	ttggatttcc	ngccctttgg	ggggggggaa	atgggcacgg	180
gngattcca	agcngntcaa	ggttccggct	tgcggacggt	taacacaant	aggtttctca	240
tctagattgg	ccngcgttgc	ggttgagcat	ccggaaaaat	tgagattgtg	tcggtaccag	300
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ccggcccttgc	ggctccggc	cttggggcact	tgcacatctg	gcggccagga	tgcgcttccg	420
ggatggcgcc	agcgegcgt	cgtcatcagc	gagcgtccat	gtgtcnntc	tgtccaagcg	480
cttaggagcc	tgcgtgtact	cccacgaagg	aagatgttagg	acccaaatgt	agaagcactt	540
aacatgaacg	tcaaaacgat	gaccatcac	agggcgat	atgcgtatgc	gcaatgttcc	600
aatcatggct	cataagcaat	ccgaaagtgg	ccaataaaat	atactatttt	ctaattccagg	660
gttacacagt	gaaacccctgt	ctcggaaaaat	aaacacaggg	ctggagagat	ggctcaactga	720
ttaagaacac	tgactgtct	tccagaagtc	tttagttcaa	ttccgagcaa	gcacatggtg	780
gctcacaacc	atctgtaca	gattctgggt	tatctggnt	cnactacagt	gtannggcat	840
tgaaagatnn	tacctgttagg	ttggncagct	aaaaaggatc			880

<210> 77

<211> 864

<212> DNA

<213> Rattus norvegicus

<400> 77

aatttaant	tgttggnata	anggcttgnc	catacccttc	ctnttggttt	ccctaagtaa	60
cagccaatttgc	ggggagaant	tttntgtcag	tatcatat	ttcggttaggg	aacggaggcn	120
caggaantga	tccntrttgg	ttacagtcat	tttagcatag	gntgacagt	ggngaccaan	180
tnatcttgc	gtgttggaa	gagggggan	taaggntgaa	gcttttgat	ccnttgc	240
ccttggatc	gggaantccc	ttaaaccac	cccttttgc	gttgaattgc	accaaccaga	300
ttcttccagt	ctgcttgagg	angacaggac	ttcattgtct	tggaggggg	caggagggtt	360
gggagttgac	tnnacagggc	tcagggattc	ttttagaagg	gtcaagggtt	atggcttccc	420
ccccccccc	ccaggtcaga	cactaaagt	tcttaagggcc	ctccataactt	gccgctcccc	480
caacnttggat	gaagccggcc	attaggcagg	gaccgtctt	gggagaggcc	aagccctctg	540
gctacttgt	ggatttccct	taagcaagac	ttcctctct	cttcaggac	tcctgtcaaa	600
caagagggtc	cctggcttag	agtttggag	ctgcaggcag	aacagacatt	ccccgatgac	660
tcacaacgtt	ggaactctgt	ggcccagcag	aatggggat	ggctttctgg	tcagtcaagg	720
tcaactggga	cactcactt	gagacaggga	ggcaaggggag	aaacaggtca	gaggttagaga	780
gagctcagtc	ccagggactc	acggttggat	ccctaagggt	cgctaggag	aggnttttac	840
attcggttng	gcaagctaaa	agag				864

<210> 78

<211> 874

<212> DNA

<213> Rattus norvegicus

<400> 78

gaggttggac	cacaaggagn	ttggngggaaa	atnnaaaagt	caacctatca	gggtgtcttt	60
tagtttggaa	cagaggcttgc	ggcagaaaata	tgggcaagta	ttaggaaagt	acaagggggaa	120
atgttgtcaa	cgcgnntttt	ttcccagtt	ttgnactgtat	cccnccagga	tgttttccca	180
cntatgtat	ggaaccnctt	ctttcaggaa	gccattntna	ncntatggnt	tgcaaccct	240

ttggggtcgc aacagcagg	attaacatta ggattcataa	cgn tagcaaa	atnacagtt	300	
tggagtagca atgaaaataac	tctatgntt ggagggtcac	cacaacanga	ggacggtat	360	
cacaggntt tagcattagg	aagggtgagg accttatttc	agagtgtcnt	gacaatcntt	420	
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tttttcattt ttttgtgtgt	tgtgtgtgt	tgtgtgtgt	tgtgtgtgt	tgtgtgtgt	780
tgcgcgcgca cgttaatatg	ccgctcagaa	tagtctaaaa	ctgctggct	tgaaagacnt	840
ncacacctgtatg	gtttgggcnat	gctaaaagag	tatc		874

<210> 79

<211> 886

<212> DNA

<213> *Rattus norvegicus*

<400> 79

attttttaat	tgcagcaatc	ctcctgcctt	ttttcttggt	tgttaantca	caggatnttt	60
gcacacttga	ggttgaantt	gcagcaatcc	tcctgtttt	gttnttggg	cgttggatt	120
atagtatgtg	cataaacactt	gagcagtaac	tgtttcttc	aatctcattt	atctcagaag	180
ttcccccttgn	tgattcagac	gttattaatt	aggcaaacca	atgttgattt	tcattaccca	240
tgagttgctt	ggcttgtgag	atgcatactg	tgtgttcgtg	aggcacntac	tgtgaggcat	300
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tcccgtctca	aaacaaaatg	aagaagtaga	gagatttagt	ttaataagca	actgaggccct	480
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aagtccaaact	tctgtttttt	cttccttccc	cgcaacatta	ggaatgactt	ctaagagngc	840
tgttqaaaga	cttcacactg	taggttggc	aagctaaaa	gaggat		886

<210> 80

<211> 865

<212> DNA

<213> *Rattus norvegicus*

<400> 80

tggaggtaaa	agtcacaagn	ttttcaaggg	tttgagatga	cagttcaacg	tgagnatnng	60
acaaggatgt	attcttgttn	acaggaaagn	tccccatccc	accaananac	accgtgttca	120
ggcccantgc	tcaagactcc	ggcgccagc	gaagggcaaa	cggccactga	ttggaaagnt	180
gcagtttaaa	gacatgtccc	aggaacttgt	anccttgtt	gactggactt	agccttgcaa	240
ntctgtctga	agcataaacnt	gntgctgtct	ntgggcgagc	atttatgtgc	cccaacttgag	300
acccatctca	ggacacgcag	gacacgttcc	agtggagctt	tccctccaga	gagaggtgtt	360
agggncatc	agttagcttc	caaggacagg	ggaccagaac	ggtgaaaaca	aaccagggtct	420
gtgaaggaga	gcagggcggg	ggggggggga	ggggggggcgc	tctntagaat	agattgaaac	480
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gcttgccat	ctcagcaagt	gtcacctcgc	tgccaggaca	caagtttctt	aaagcttatt	600
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gggaacctgt	gcgtttaag	gtctgagttt	cacacaggct	gctcaggaag	gagcttagagc	780
tccaaatagg	agctgtgatc	aggctgtgtg	tgtgtgcctg	gtgaaagact	ttnacctgtta	840
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<210> 81

<211> 859

<212> DNA

<213> Rattus norvegicus

<400> 81

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cataccaaa	agtccctact	gttatccaa	tttagtaggct	ggctgccaat	agttgtccat	540
acagagtcc	tgctgtgt	gccatccnta	ctgttagtaaa	cagtcatcca	aagctcagga	600
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gaaaggaca	caggccaaag	gtgggaggcc	ttagataaag	gcccatcatg	ctcaggaaag	720
gattntaca	gatctttag	ggaagttaca	atcaaattca	tacccatcag	cagagctcag	780
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<210> 82

<211> 1021

<212> DNA

<213> Rattus norvegicus

<400> 82

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tttttttag	nggaattttg	ggttcaant	gngttaccc	taagtaaccc	cattttgcan	180
ggcatggaaa	atacctaann	tggatngaa	agttcanatn	gaggtcagga	angngntgaa	240
cagggtngac	cggttngacc	gttggaccc	tgagancat	cagatnttc	ccagggttncc	300
ccaaggactt	gaaatgaccn	tgtnccttat	ttnaantacc	caatcagttg	gtttctcgct	360
tctgttcg	cgtttttgtt	cccggagttc	aataaaggag	cccaacaccc	ntcantrnggg	420
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tacccgtcag	cgggggtctt	tcaaaactgca	gttctcaagt	aagctcaacc	atccgagggt	600
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tatctgatgg	gattntaagt	ccctggcag	acccgggtt	gtgggcctga	agcttgagtt	960
ncaggagact	tagtgggcca	tgggattctt	tttagatccc	gatatggna	aacttaaact	1020
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<210> 83

<211> 1013

<212> DNA

<213> Rattus norvegicus

<400> 83

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acactcgtgt	gggncttttc	aaaacantgt	ncnntggata	cncagacact	cnnncnagnn	180
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nnggcacata	tntntgacac	nngngtata	nngnctctn	ggnganacat	ttgntrncga	300
caaaaancn	tggagattn	tctacncaat	annctanttt	tcacagggna	gcncntgtnn	360
anacncncac	ctnacacaan	tnnggnntgt	ntcagagng	attttanctc	nntrngncana	420
cccgnttntg	tgnnccaaan	tnttggtttc	caagacat	agtggncat	gnnactctnc	480
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tcacagat	gtgtntatnt	cnnacanaca	aatntgcnn	actccctctg	tgtataaact	600
aatanacggg	ngggtaaca	tnngccnch	gttgnncagt	natacngna	aacacactcn	660
caaggcgtnc	aannttttnc	ntctacacn	cncncccgan	gggnncngnc	acaaaatgtgc	720
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cattttttna	aaaagngttt	accntggcc	ccntntttt	cnaaaaaatt	tgnccccgn	960
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<210> 84

<211> 1002

<212> DNA

<213> Rattus norvegicus

<400> 84

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ttagagggtcc cacttgnat caggttattc tggtgccttg ggtcaagcaa acagccnatc	180
aggattgtga ttatngnat aaccattta cctnacagcn ggggaaan ccaangggag	240
gcttggagaa acggcttggg gttcataaa ctcttgaata cataccttgg gtgattcaaa	300
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gaaaagcatt gaaaactcaa accataccac tatcagttc agcttaata taaaattagct	420
ttctaagttc agctgaccac ntttcactg gaccttcaact gatcacakag ggaagatata	480
tttcaacaa ttacaaagac atttctgggt tggactatgc attccttgg gccagattct	540
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<210> 85

<211> 1031

<212> DNA

<213> Rattus norvegicus

<400> 85

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cttacaaggg aaatattattt ttcacaatgg ttttagaggtt ccactgttac aagtattctg	180
ttgctttgggn ccangtcaaa cagcccatca ggatgggtat attagaatta accatttatac	240
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gcattccctt gggccagatt ctacatcctt tttttatggc agaattttt acggttccctg	600
taagattgtc agttttccctt aggaatcca taaagcttta aatgccttctt aatagccaa	660
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taaaagctgtt acatgtgatt ttctctgtt tacctttat actcattttt tttgttattt	960
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<210> 86

<211> 1039

<212> DNA

<213> Rattus norvegicus

<400> 86

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ccntggata anaagtggaa tcattgacag ttttgggtt cttttnncat ccccatgngg	180
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gnggagtattt agcaaaattttt actgacttgc tcacttntgc aaantgatgt ctgatttccg	360
aagaatccca gtcctcggg acatgaaagg gagatgttac cttgagttca tggtaggag	420
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tgtgtatgtt ctatcncgtt gaggagaga ctttgcactc tgcctctgaga aggccaaact	540
gttaggcaga cacttagaga atatatgtca tggccaaaga catccaccca acaagtcttc	600

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agtaacaaag	cactaaacag	aaaggggtt	aagagactgg	tcagtggctg	agagcttta	660
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atgcctctgg	cctcaggaga	cacctgtga	ctccccacca	gacacatata	ctaaaaata	780
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aggcagcaca	ggcctaacag	cccataatgt	gtgctattct	atcaatagtg	ccaagtattg	960
acatggacta	ttcaaaaggc	ccaaaagtta	aatggccag	aagtncaaca	taaagnccgg	1020
cnagctaaaa	gagatcnctc					1039

<210> 87

<211> 1058

<212> DNA

<213> Rattus norvegicus

<400> 87

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tnttggccag	ttgggatttt	gattgantgg	gaacccccc	gnnttaata	agcctttgg	180
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attgtcataa	cttcttgaa	agttttagga	cttggacgga	cagaagacat	gatcattat	420
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acattgggtt	ttcttgatt	agctatccac	tcttgcctc	accctccac	cccctaata	540
ccagttac	tgacgatgt	ggtattttc	tctgaacaca	ttcttctt	ggatgttaaa	600
gtgcattt	acactgttt	taggacact	gtttaggccc	gggtggggg	attgcccacag	660
aagcttgacc	ttagaaggt	gagactctgg	aaggctgaga	gagatgagat	ctgtcaaaga	720
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agcagggcag	acagtcttct	gatgatttct	ctgccttcaa	actgaggt	nn actcttgaaa	1020
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<210> 88

<211> 1043

<212> DNA

<213> Rattus norvegicus

<400> 88

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ccttngaaaa	ngagttgttag	tnttaancgg	caaacaacca	ccggtttag	cgtggtttt	180
tgttgcaagc	ngcggtagg	gcccgggggg	ggatntaagg	agatccttn	nttttctt	240
ggggctgtac	gnntcatgtt	gtgtggatt	ntgagcgg	tttacaat	acngatttt	300
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<210> 89

<211> 454

<212> DNA

<213> Rattus norvegicus

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<400> 89

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gcagggtctc	aaggcacaca	aataacgcca	ctggaatgtg	gtgcagggtc	ccgggtgggg	180
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cagtttgtg	cagctcaagg	gcacaaggnt	agtgcctt	ncttggncnt	gaggcactnn	420
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<210> 90

<211> 873

<212> DNA

<213> Rattus norvegicus

<400> 90

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<210> 91

<211> 876

<212> DNA

<213> Rattus norvegicus

<400> 91

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<210> 92

<211> 459

<212> DNA

<213> Rattus norvegicus

<400> 92

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ctggctgagg	ttgagtgtat	caagtaatca	actggcagta	ccctntgggg	agtggccctgt	720
gttttcc	tcccctt	gggtgagaaa	tccttaggg	gtgggagcca	aggcttaggc	780
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agaa	gaaacgg	gctgg	acccactt	ggcagcagg	tttcttccc	1440
tag	ccctt	tttgc	atactt	ctgcacacc	ctcacc	1500
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aagg	cc	gggg	gggttgg	actcagg	cagcgt	1920
gggg	cc	gggg	gggg	gggg	ggggcccc	1980
gat	cc	gggg	gggg	gggg	accacag	2040
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cc	cc	gggg	gggg	gggg	cc	2940
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<210> 94
 <211> 2161
 <212> DNA

<213> Rattus norvegicus

<400> 94

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tgtgtgtgt	tgtgtgtgt	tgttagata	acgaactact	gacaattca	rgarcataaa	2040
cattatggaa	attttttgc	gtatgtcatc	attttaattt	taaaagatgc	tttattttct	2100
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a						2161

<210> 95

<211> 824
 <212> DNA

<213> Rattus norvegicus

<400> 95

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atgtgtcg	gagaaaacccn	ttcagtnntg	tgcaatttgc	tcgcacagcg	ttaggaccgn	180
ttccctatca	cttgcgcag	cggacatcata	gntatttgagc	cntgnatcat	ttatggnaca	240
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aattcgttgc	ggcgactcta	accaggaagc	ctaatcccttgc	agattcccgg	gacactgggg	420
caggcgttct	aaaaacacgt	ttgtggggct	tcagtccttc	gtgcgggttcc	agtccgggtc	480
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ggcccttctc	ggtgcacccacg	caccccccga	tcaaccccgaa	ggatgagcat	aggggtgtatt	660
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cactataaag	gaggccagg	ccaaggactg	gcctcttgc	gctcacgagg	tcaagacgcga	780
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<210> 96

<211> 774

<212> DNA

<213> Rattus norvegicus

<400> 96

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gaggggaaa tgagcacng gcantccaa	cgntcaaggt cccgnttcgg acggtcacac	120
antaggtnt catntggatt gccnngnttc	cngtggcat cgggaaaan tgagactgtg	180
tcggtagcc agnttaggtg cccntccctt	ccngccccgg ctttttggc gccttgcgat	240
ccttccgaa cgggcccnnntg	gcgttccgc ctnggcact tgcacatntg	300
atggcgcttc cgggatggcg	cgagcgcgac tacgtcatca	360
tctgtccaag cgcntaggg	cggagcgtcc atgtgttctt	420
gtagaagcac ttaacatgaa	cctgcgcgta ctccagcaa ggaagatgta	480
gcgcaatgtt ccaatcatgg	gcgatcc acagggcgat atatgcgcatt	540
tactaatcca gggttacaca	atccggaagt ggcaattaa atatactatt	600
atggctca	gtgaaaccct gtctgaaa ataaacacag	660
aagcacatgg tggctcacaa	ggctggagag atgactgtcttccagaag	720
gtgtactcgt attgaaagt ncccacctgt	ttttagtngtga gacaactaca	774

<210> 97

<211> 248

<212> DNA

<213> Rattus norvegicus

<400> 97

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tagctcaggc	ttgttttggaa atcaggatcc tgaccctcag	180
gtggngacaa	aatattttac gtgccttga aagacttca	240
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<210> 98

<211> 880

<212> DNA

<213> Rattus norvegicus

<400> 98

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taaggcgggt tcaaaca	ttggatttcc ngcccttgg ggcggggaa	180
gngcattcca	agcngntcaa gttccggct tgccgacggt	240
tctagattgg	taacacaant aggtttctca	300
ccngcgttgc	ggttgagcat cgggaaaat tgagattgt	360
aggttagatg	tcgggtaccag ggccttcctt	420
ccggcccttgc	ccngccccg gttcctg	480
ggatggcgcc	tcgttgcact tgacatctg	540
cttaggagcc	gacgttccat gtgtcnntc	600
tgccgtact	tgccgtact cccagcaagg	660
aacatgaacg	aagatgtagg accaaaatgt	720
tcaaaacgat	agaagcactt gaccaatcac	780
aatcatggct	agggcgat atgcgcatt	840
gttacacagt	gcaatgttcc	880
ttaagaacac	aatatatttata	
gctcacaacc	ctgttgcact	
tgactgtct	ttccagaagtc	
ttttagtngtga	ttttagtngtga	
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tacctgttagg	ttggncagct	
	aaaaaggatc	

<210> 99

<211> 864

<212> DNA

<213> Rattus norvegicus

<400> 99

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ggggagaant	tatcatattt ttcgttaggg	180
caggaantga	ttacagtcat tttagcatag	240
tnatcttgcc	gntgacagtt gnggaccaan	
gtgttggaaag	gagagggan taaggntgaa	
	gctcttgagt	
	ccnttgangc	

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ccttggaaatc	gggaantccc	ttaaaccaac	ccctttgcc	gttgaattgc	accaaccaga	300
ttcttccagt	ctgcttgagg	angacaggac	ttcattgctn	tggagagggg	caggagggtt	360
gggagttgac	ntnacaggc	tcagggattc	ttttagaagg	gtccaggttc	atggcttccc	420
ccccccccag	ccaggtcaga	cactaaagtg	tcttaagccc	ctccatactt	gccgctcccc	480
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caagagggtc	cctggcttag	agtttggag	ctgcaggcag	aacagacatt	ccccgatgac	660
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<210> 100

<211> 874

<212> DNA

<213> Rattus norvegicus

<400> 100

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tggagtagca	atgaaataaac	tctatgnnttgc	ggagggtcac	cacaacanga	gggacggat	360
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<210> 101

<211> 886

<212> DNA

<213> Rattus norvegicus

<400> 101

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atagtagtgt	cataacacttgc	gagcgttaac	tgttttcttc	aatctcattt	atctcagaag	180
ttcccttgc	tgattcagac	gttattaaatt	aggcaaacc	atgttgatttgc	tcattacc	240
tgagttgc	ggcttgcgt	atgcatactg	tgtgttgcgt	aggcacntac	tgtgaggcat	300
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tcccgtctca	aaacaaaatg	aagaagttaga	gagatttagtgc	ttaataagca	actgaggcct	480
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<210> 102

<211> 865

<212> DNA

<213> Rattus norvegicus

<400> 102

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ggcccantgc tcagagctcc	gggcgccagc	gaaggggcaaa	cggccactga	ttggaaaagt	180
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<210> 103

<211> 859

<212> DNA

<213> Rattus norvegicus

<400> 103

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ttgtgcacgg	gaggccagc	tcancnnct	tggagntt	acatccagca	180
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aacccttgag	ttaatttcc	agggtcaact	gtatttgaa	agtataaatg	360
aagaataaaa	ttttagat	gttagatca	cactgttca	aatagctaa	420
cntgtctct	taatgtt	aatcatctt	tactcaacg	tgtccacaat	480
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<210> 104

<211> 883

<212> DNA

<213> Rattus norvegicus

<400> 104

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<210> 105

<211> 987

<212> DNA

<213> Rattus norvegicus

<400> 105

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taaaggatgg ctaataaga cgtcttagaa atgtccacat tatattggat caacaaacgc	900
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<210> 106

<211> 1031

<212> DNA

<213> Rattus norvegicus

<400> 106

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<210> 107

<211> 1138

<212> DNA

<213> Rattus norvegicus

<400> 107

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nangannnaa nccgggnnaa ncannncagnn gggaaacagc ccagagagat aggacancaa	180
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agaanagnnc aacnnnnnca nnnngacccn gaanagggnn nnngaacngc nancnnccna	300
gnngcngan cnanacacga cngaaagagac gngngcngaa naganacncn gaanngnaac	360
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gcangnanch gacnaggaaac gacngnaagn gcnagnnac ganngcaga nnanangaaa	600
cacgnnnnan acannnacn ancgacgg nncaggaaag ngngcnaacn gaggnngngcc	660
aanaaganaa nngngagann aaaaaaaaaa ngngngncan gcagnanaaa accgagnncn	720
nnnnnnnnna gaganagaac gagannnang nncgannac gcgnacaaga anggaaannn	780
cgnangacgc nncggaaacaa ngacnnnnnnaa anncagnn anccaacnag gnaannnaga	840
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<213>	Rattus norvegicus					
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<212>	DNA					
<213>	Rattus norvegicus					
<400>	109					
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ccaaatttt	nanttttaga	aaagtcttt	ggtnaata	cagcn	tgtatggagca	180
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gctggccact	ataaggccag	ccagactcgc	acacagtcca	tccctcgac	cactctttt	960
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gcggtagact gactgcttcc cctctcgctt ggagttgacc ttgcactag agggcaacag	300
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gctggtagan ggttcagcac acataccaga gttacagatc acgtgccana anggcaaaact	420
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ccagggctgc tnggctgtn aaaaaaanc caggtaagg ganccatgg gngggaaanc	900
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tggcccctca ggaggnttca nggaaanc cattccttcc ttgccaatca aaagccccat	1020
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<210> 111

<211> 1069

<212> DNA

<213> Rattus norvegicus

<400> 111

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caaaattcta cttttggaa tcagcntatn tcatcaggat ttagccctgt gtgnntaacc	300
tgtggagacc cttttcacag ganttgcctt agaccattt aaacacagta tttatgtcan	360
gattcataac agtagcaaaa atatagttttaat gaaacggcata cgaaatact ttatgggttg	420
agcgtcacca caacatgagg aatgtattaa tccgcagttat tagagaggc gagancact	480
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acactgatct ctggctggta gagggttcag cacacatacc agagttacga gtcacgtgcc	660
agaagggcaa actgaacacg gaatttagagg gaactcgatg tctccggctt gcactggct	720
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ctctactgg ggcgtccctc taagatctgt ccactccttgc tntaggggtt aagcccttgc	1020
tgccctgaaa gatttncacc tggatgttgg gcaagctaaa agagangcc	1089

<210> 112

<211> 1058

<212> DNA

<213> Rattus norvegicus

<400> 112

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tgggaaccng acgggtttaa gntaccgggt ttcccnntt agtccnttgg gttccctntc	120
cgacccttcgg ttaccggta ctgcccncctt ttccctttgg gagggtgggn ttttcatag	180
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atttgcgtt ttgttgaatc cgttactttt nggaaaggag tttgttagttc ttatccggc	480
aaacaancca cngttagtntt cgggtgggtttt ttgttgcgca agcagcatg tacgcgcaga	540
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gtggaaattgt gacggatca caatttcaca cagaattttt cttagaaaaa tctgtccctc	660
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tatattcctg agcattgcct atcccttaag gtactacaaa atttgggagt gaggctcagc	960
aaactatttt aacatgcctc tccccccaa ctactcaaga ttccccgtgc acagttgaaa	1020
gnttnccac ctgnaggtgg gccaaagcta aaagagat	1058

<210> 113
 <211> 1046
 <212> DNA
 <213> *Rattus norvegicus*

<400> 113	
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anggggann naanggcana annnatggac gagagtnaan ancgcnangn agaagantna	120
aaantcncca nntggngccc caaatnnnc aattganca aancnntaga ggnncnncaag	180
acnaatgggc actntganna gancngcca gaagncaagn ggggannnt catagnnaca	240
tggnnaaaat aaagntntgt aaacccggan tggcaatnga aaccagcaaa gacccatgaa	300
cgtgagngan accagttgga aacaatgaan nnantgggt antnacagga atgnggthan	360
gacgcnaggt gancccaaan aggcaacncc attgaaagcc ttcnccncca tggaaatact	420
gtanntaaaa caaacaaca aatnacaaaa anaaaaaacc caaagcttaa gtggagtgcc	480
cnttccagnt agccacccnnn taagaactgt aatcgcacc ntccancgcc agatgcaggt	540
aaggnaggat tacaggnatn tcggagggct caggaggaa tgggtcncaa nntgagctga	600
ggcncnnggtg antncgcta cntcgnaaaa aangagaagt catgtggac gnatgtgt	660
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cataatagna ttgttacang atncnnngact ttanaaaaan caaaatccta aatcctattc	780
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ctaggcaagc gctctaccag tgagctaaat cncaacccc cacagntgcc tcntntgatt	960
gnaggtntcn tatcccnntc ttttggca agntttctg ggcccnntga aagtgaannnc	1020
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<210> 114
 <211> 1083
 <212> DNA
 <213> *Rattus norvegicus*

<400> 114	
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ttgnntgggg tgaattcccg ccntngntt gaggaggnaa ttatnttgta gaaattttatg	180
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gcccagtgtg ctcaacccct tggaaacccct ttaacaggat ttgcttggnc catntgaaac	360
acagtttta tggcaggatt cataacagta gaaaaantt agttatgang cagcaagaaa	420
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aaggccagcc agactgcgac acagtccatc cctcgtacca ctcttttgc gtttcattgt	960
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gtttaaggcct tntgtcccc tggaaatggatc tttttttttt gttttttttt tttttttttt	1080
ttt	1083

<210> 115
 <211> 913
 <212> DNA
 <213> *Rattus norvegicus*

<400> 115	
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cnaanttccc tttggacgcc ntttacaaga ttggccngtgc tgtaacctt gggcccttta	180

acaggattnc ttggccnntt gaaacacgta tttatgtcag gnttnttaccg tngcaaant	240
ngttttgagc agcaacgaaa tcactttatg gttggaggc accacaactt gaggatgtat	300
taatccgcag tattagagag tcgagaacca ntatctttaga ggatcggtag actgtatgtt	360
cccnnttngc ttggagttgn cttnccacta gaggcaacag catcagtatt gttcccagt	420
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agtccgggac gtccaggcaa caaggcgtg gaaagtggg aggctgggag gtgtgtttgc	660
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gctaaatgag atc	913

<210> 116
 <211> 1123
 <212> DNA
 <213> Rattus norvegicus

<400> 116

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aaatgaggnt aattggntt gaaangcnta tcaggcattc caaattntta aatttccctt	180
ggccagagat tggggaaaat ttncccgga ntccagnntt aggttnttgg gaaaaacggn	240
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acagggccaa accnttgcgt taaaanaagt taacttgcgc ccccaactcan gcgtcagtgg	660
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aaacagggtt cctccagtcg tgcgacgttcc cccgacttcc gcacccttt taaggcctgt	960
gttgcggatc cgcgcggccca tcacgcattt catcaggtt ttactgtgtg gaaacacgt	1020
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aattgaaaga cttttnccctg taggnanggg nagctaaaaa gat	1123

<210> 117
 <211> 1116
 <212> DNA
 <213> Rattus norvegicus

<400> 117

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aaaaaaacnnnt gttcttnaat gcaaggtant tgggggttat tattntgaaa gcaactaat	180
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ttggnggtgt gggnttaaaa cccttggtnn ccagggttcc antgggttca gccccttga	300
gnnggntccc ctttccccgg gaatnggntt gaaccggaaa ttgaacattt tgcaccctt	360
tccggngggcc ctaaggattt gcagcnccag ttgcggggaa gggtaattt cttgcacccncc	420
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atccagatc	tgaggnaaat	tggatggttc	gggtgtctat	gttnacntaa	gacctgtttt	960
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<210> 122

<211> 970

<212> DNA

<213> Rattus norvegicus

<400> 122

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caactgagat						970

<210> 123

<211> 884

<212> DNA

<213> Rattus norvegicus

<400> 123

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<210> 124

<211> 855

<212> DNA

<213> Rattus norvegicus

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<400> 124
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<210> 125

<211> 1059

<212> DNA

<213> Rattus norvegicus

<400> 125

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gtttaaaa	ataaaat	ttttt	tttttt	ttgtgttca	ttgtgttca	900
tttgataaa	aaaagag	ttttt	ttttt	ttgtgttca	ttgtgttca	960
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<210> 126

~~2110~~ 120

<212> DNA

<213> Rattus norvegicus

<400> 126

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<210> 127
 <211> 960
 <212> DNA
 <213> *Rattus norvegicus*

<400> 127

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